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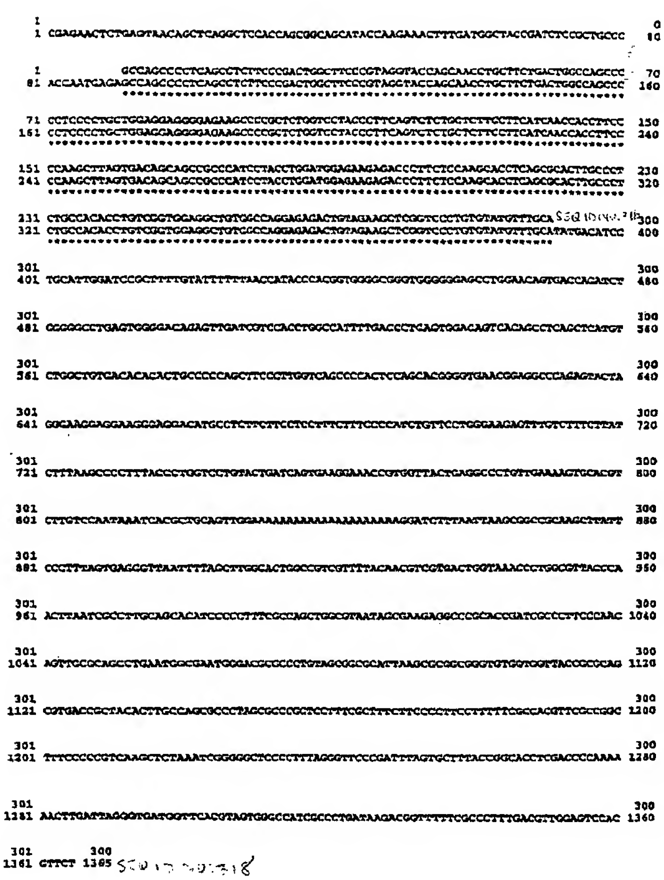
(54) Title: HUMAN GENES AND GENE EXPRESSION PRODUCTS XVI



(57) Abstract: This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variant thereof, to genes corresponding to theses polynucleotides and to proteins expressed by the genes. This invention also relates to diagnostic and therapeutic agents employing such novel polynucleotides, their corresponding genes or gene products, *e.g.*, these genes and proteins, including probes, antisense constructs, and antibodies.

WO 01/72781 A2

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HUMAN GENES AND GENE EXPRESSION PRODUCTS XVI

Field of the Invention

The present invention relates to polynucleotides of human origin and the encoded gene products.

Background of the Invention

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

Summary of the Invention

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-316.

Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Brief Description of the Figures

Figures 1A-1B is a comparison of SEQ ID NO:315 and clone H72034 (SEQ ID NO:317).

Figure 2 is a comparison of SEQ ID NO:316 and clone AA707002 (SEQ ID NO:318).

Detailed Description of the Invention

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA genomic sequences, and genes corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants. The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA

encoding a full-length gene product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOS:1-316; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicted.

The invention features polynucleotides that are expressed in human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-316 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS: 1-316.

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC.

Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-316) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOS:1-316. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOS. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, e.g., probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-316, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete

sequence that is being compared. Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOS:1-316. For the most part,

fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-316.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-316. The probes are preferably at least about a 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOS:1-316, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-316. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the

polynucleotide sequences as shown in SEQ ID NOS:1-316 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-316, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in USPN 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-316. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) can be performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.,* 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al*., such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al*., WO 95/04745 and Gruber *et al*., USPN 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant

polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) *15*:890-893; Edwards *et al.*, *Nuc. Acids Res.* (1991) *19*:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. The method uses lock-docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT)(see, e.g., WO 96/40998).

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOS:1-316) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS:1-316; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOS:1-316, preferably the entire sequence of at least any one of SEQ ID NOS:1-316, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS:1-316 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS:1-316.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotides (*e.g.*, a polynucleotide having a sequence of one of SEQ ID NOS:1-316), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOS:1-316 can also be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, *e.g.*, Stemmer *et al.*, *Gene (Amsterdam)* (1995) *164(1)*:49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) *370*:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in USPN 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOS:1-316 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in USPN 5,641,670.

<u>Identification of Functional and Structural Motifs of Novel Genes Screening Against Publicly Available Databases</u>

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co.,

San Diego, California, USA. Databases include GenBank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST 2.0, available over the world wide web at a site supported by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health. See also Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) *70*: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases. Incorporated herein by reference are all sequences that have been made public as of the filing date of this application by any of the DNA or protein sequence databases, including the patent databases (*e.g.*, GeneSeq). Also incorporated by reference are those sequences that have been submitted to these databases as of the filing date of the present application but not made public until after the filing date of the present application.

Results of individual and query sequence alignments can be divided into three categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value. The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11

amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al., Proc. Natl. Acad. Sci.* (1990) *87*:2264 and Karlin *et al., Proc. Natl. Acad. Sci.* (1993) *90*. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al., Nat. Genet.* (1994) *6*:119. Alignment programs such as BLAST program can calculate the p value. See also Altschul *et al., Nucleic Acids Res.* (1997) *25*:3389-3402.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST 2.0 (see, *e.g.*, Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402) or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More typically, the p value is no more than about 10^{-5}; more typically; no more than or equal to about 10^{-10}; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2}; more usually; less than or equal to about 10^{-3}; even more usually; less than or equal to about 10^{-4}. More typically, the p value is no more than about 10^{-5}; more usually; no more than or equal to about 10^{-10}; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*, polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) *24(14)*: 2730-2739. MSAs of some protein families and motifs are publicly available. For example, the Genome Sequencing Center at thw Washington University School of Medicine provides a web set (Pfam) which includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) *28*: 405-420. Other sources over the world wide web include the site supported by the European Molecular Biology Laboratories in Heidelberg, Germany. A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) *9(3)*:249-251. Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) *266*, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney *et al.*, *supra)*. Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351 and Higgins *et al.*, *CABIOS* (1989) *5*:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) *25*:351. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) *48*:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) *2*:482. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from

two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

Identification of Secreted & Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) *78*:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) *157*: 105-132; and RAOAR algorithm, Degli Esposti *et al.*, *Eur. J. Biochem.* (1990) *190*: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

Identification of the Function of an Expression Product of a Full-Length Gene

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al.*, *Tet. Lett.* (1981) *22*:1859 and USPN 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiruam disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard

phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt, more typically 50 nt; even more typically 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al., supra*. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect. One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme, as well as therapeutic uses of ribozymes, are disclosed in Usman *et al., Current Opin. Struct. Biol.* (1996) *6*:527. Methods for production of ribozymes, including hairpin structure ribozyme fragments, methods of increasing ribozyme specificity, and the like are known in the art.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) *17*:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al., Eur. J. Biochem.* (1997) *245*:1.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to

"hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) *329*:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS:1-316 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST 2.0 using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid

sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST 2.0 algorithm, with the parameters described *supra*.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, e.g., Go *et al*, *Int. J. Peptide Protein Res.* (1980) *15*:211), the thermostability of the variant polypeptide (see, e.g., Querol *et al.*, *Prot. Eng.* (1996) *9*:265), desired glycosylation sites (see, e.g., Olsen and Thomsen, *J. Gen. Microbiol.* (1991) *137*:579), desired disulfide bridges (see, e.g., Clarke *et al.*, *Biochemistry* (1993) *32*:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) *7*:1379), desired metal binding sites (see, e.g., Toma *et al.*, *Biochemistry* (1991) *30*:97, and Haezerbrouck *et al.*, *Protein Eng.* (1993) *6*:643), and desired substitutions with in proline loops (see, e.g., Masul *et al.*, *Appl. Env. Microbiol.* (1994) *60*:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-316, or a

homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-316. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-316. The length and number of polynucleotides in the

library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-316, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the gapped BLAST (Altschul *et al. Nucleic Acids Res.* (1997) *25*:3389-3402) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt A variety of comparing means can be used to accomplish comparison of sequence information from a sample (e.g., to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but arc not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOS:1-316 , *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-316 is represented on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of

applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-316.

Utilities

Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al*., *Meth. Enzymol.* (1987) *155*:335; USPN 4,683,195; and USPN 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook *et al*., "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a

solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected.

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in USPN 5,783,387. An exemplary mapping method is fluorescence in situ hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences (see, e.g., Valdes *et al.*, *Methods in Molecular Biology* (1997) *68*:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) *33*:63-99; Walter *et al.*, *Nature Genetics* (1994) *7*:22; Walter and Goodfellow, *Trends in Genetics* (1992) *9*:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at sites supported by the Stanford Human Genome Center (Stanford University) and the Whitehead Institute for Biomedical Research/MIT Center for Genome Research. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at a site supported by the Center for Statistical Genetics at the University of Michigan School of Public Health. In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product. As would be readily apparent to any forensic scientist, the sequences disclosed herein are useful in differentiating human tissue from non-human tissue. In particular, these

sequences are useful to differentiate human tissue from bird, reptile, and amphibian tissue, for example.

Use of Polymorphisms. A polynucleotide of the invention can be used in forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

Antibody Production

Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Methods for production of antibodies that specifically bind a selected antigen are well known in the art. Immunogens for raising antibodies can be prepared by mixing a polypeptide encoded by a polynucleotide of the invention with an adjuvant, and/or by making fusion proteins with larger immunogenic proteins. Polypeptides can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Monoclonal antibodies can be Monoclonal antibodies can be generated by isolating spleen cells and fusing myeloma cells to form hybridomas. Alternatively, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, e.g., at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the

invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of the invention in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies, antibody derivatives (e.g., single chain antibodies, antibody fragments (e.g., Fab, etc.)), according to methods well known in the art.

Polynucleotides or Arrays for Diagnostics

Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression, e.g., to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocelllose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734. Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a polynucleotide between a test cell and control cell (*e.g.,* cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) *8*:217; and Ramsay *Nature Biotechnol.* (1998) *16*:40.

Differential Expression in Diagnosis

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to

a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (*e.g.*, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in USPNs 5,688,641 and 5,677,125.

A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.,* breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.,* cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease. It should be noted that use of the term "diagnostic" herein is not necessarily meant to exclude "prognostic" or "prognosis," but rather is used as a matter of convenience.

The term “differentially expressed gene” is generally intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

"Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. “Differentially expressed polynucleotides” is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

"Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*,

ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, e.g., WO 97/27317).

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-316 The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-316, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-316 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes,(*e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.* ^{32}P, ^{35}S, ^{3}H, *etc.*), and the like. The detectable label can involve a two stage systems (*e.g.*, biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

<u>Polypeptide detection in diagnosis.</u> In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (*e.g.*, using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (*e.g.*, biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, *e.g.* fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can of qualitative or quantitative detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

<u>mRNA detection.</u> The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One

of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (e.g., Velculescu et al., *Science* (1995) *270*:484) or differential display (DD) methodology (see, *e.g.*, U.S. 5,776,683; and U.S. 5,807,680).

Alternatively, gene expression can be analyzed using hybridization analysis. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (*e.g.*, mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

<u>Use of a single gene in diagnostic applications.</u> The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled

primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see e.g., Riley *et al.*, *Nucl. Acids Res.* (1990) *18*:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) *58*:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.).* The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

<u>Pattern matching in diagnosis using arrays.</u> In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOS:1-316. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of

polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in GenBank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more. Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The

sequence information can then be stored in a format (*e.g.*, a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can be compared to previously generated and stored REPs.

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Methods for collection of data from hybridization of samples with a reference arrays are well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label using, for example, a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in USPN 5,631,734. A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) *6*:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (*e.g.*, a test sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.* data deviating from a predetermined statistical distribution,

and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays), design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

Diagnosis, Prognosis and Management of Cancer

The polynucleotides of the invention and their gene products are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression

levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides of the invention can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. Furthermore, a polynucleotide of the invention identified as important for one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide is differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following "TNM" system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggresivity of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining

the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, e.g., polynucleotides differentially expressed in normal cells versus cancerous lung cells (e.g., tumor cells of high or low metastatic potential) or between types of cancerous lung cells (e.g., high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate therapy. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Detection of breast cancer. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows: 1) ductal carcinoma in situ (DCIS), including comedocarcinoma; 2) infiltrating (or invasive) ductal carcinoma (IDC); 3) lobular carcinoma in situ (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma;

The expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the

metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.* ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Detection of colon cancer. The polynucleotides of the invention exhibiting the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC ras, lor FAP (see, e.g., Fearon ER, *et al.*, *Cell* (1990) *61(5)*:759; Hamilton SR *et al.*, *Cancer* (1993) *72*:957; Bodmer W, *et al.*, *Nat Genet.* (1994) *4(3)*:217; Fearon ER, *Ann N Y Acad Sci.* (1995) *768*:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc.

Detection of prostate cancer. The polynucleotides and their corresponding genes and gene products exhibiting the appropriate differential expression pattern can be used to detect prostate cancer in a subject. Over 95% of primary prostate cancers are adenocarcinomas. Signs and symptoms may include: frequent urination, especially at night, inability to urinate, trouble starting

or holding back urination, a weak or interrupted urine flow and frequent pain or stiffness in the lower back, hips or upper thighs.

Many of the signs and symptoms of prostate cancer can be caused by a variety of other non-cancerous conditions. For example, one common cause of many of these signs and symptoms is a condition called benign prostatic hypertrophy, or BPH. In BPH, the prostate gets bigger and may block the flow or urine or interfere with sexual function. The methods and compositions of the invention can be used to distinguish between prostate cancer and such non-cancerous conditions. The methods of the invention can be used in conjunction with conventional methods of diagnosis, e.g., digital rectal exam and/or detection of the level of prostate specific antigen (PSA), a substance produced and secreted by the prostate.

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, e.g., USPN 5,010,175 , and WO 91/17823). Agonists or antagonists of the polypeptides if the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions of the invention can comprise polypeptides, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The term "therapeutically effective amount" as used herein refers

to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); or (2) delivered ex vivo, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories,

and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the ex vivo delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO 93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoetic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic compositions agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) *11*:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) *263*:621; Wu *et al.*, *J. Biol.*

Chem. (1994) *269*:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) *87*:3655; Wu *et al.*, *J. Biol. Chem.* (1991) *266*:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 μg to about 2 mg, about 5 μg to about 500 μg, and about 20 μg to about 100 μg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) *1*:51; Kimura, *Human Gene Therapy* (1994) *5*:845; Connelly, *Human Gene Therapy* (1995) *1*:185; and Kaplitt, *Nature Genetics* (1994) *6*:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) *3*:147 can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) *3*:147); ligand-linked DNA(see, e.g., Wu, *J. Biol. Chem.* (1989) *264*:16985); eukaryotic cell delivery vehicles cells (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with

cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN 5,580,859. Liposomes that can act as gene delivery vehicles are described in USPN 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) *14*:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) *91*:1581

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al., Proc. Natl. Acad. Sci. USA* (1994) *91*(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., USPN 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

The following examples are offered primarily for purposes of illustration. It will be readily apparent to those skilled in the art that the formulations, dosages, methods of administration, and other parameters of this invention may be further modified or substituted in various ways without departing from the spirit and scope of the invention.

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

cDNA libraries were constructed from mRNA isolated from the GRRpz or and WOca cells, which were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz cells were primary cells derived from normal prostate epithelium. The WOca cells were prostate epithelial cells derived from prostate cancer Gleason Grade 4+4. Polynucleotides expressed by these cells were isolated and analyzed; the sequences of these polynucleotides were about 275-300 nucleotides in length.

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36,

p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40}, and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 316 sequences listed as SEQ ID NOS:1-316 in the accompanying Sequence Listing and summarized in Table 1 (inserted prior to claims). Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Many of the sequences include the sequence ggcacgag at the 5' end; this sequence is a sequencing artifact and not part of the sequence of the polynucleotides of the invention.

Table 1 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER"); 3) the sequence name ("SEQ NAME") used as an internal identifier of the sequence; 4) the orientation of the sequence ("ORIENT"); 5) the name assigned to the clone from which the sequence was isolated ("CLONE ID"); and the name of the library from which the sequence was isolated ("LIBRARY"). CH22PRC indicates the sequence was isolated from Library 22; CH21PRN indicates the sequence was isolated from Library 21. A description of the libraries is provided in Table 3 below. Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention

may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

Example 2: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-316 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs, available over the world wide web at a saite sponsored by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health (see also Altschul, et al. *Nucleic Acids Res.* (1997) *25*:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Table 2 (inserted before the claims) provide the alignment summaries having a p value of 1 x 10^{-2} or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Specifically, Table 2 provides the SEQ ID NO of the query sequence, the accession number of the GenBank database entry of the homologous sequence, and the p value of the alignment. Table 2 also provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous sequence, and the p value of the alignment. The alignments provided in Table 2 are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification. The activity of the polypeptide encoded by the SEQ ID NOS listed in Table 2 can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and actual activities and functions of the nearest neighbor sequences listed in Table 2 and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to

construct a library for the full-length sequences of the corresponding polynucleotides.

Example 3: Differential Expression of Polynucleotides of the Invention: Description of Libraries and

Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including primary cells, cell lines and patient tissue samples. Table 3 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Table 3. Description of cDNA Libraries

Library (Lib#)	Description	**Number of Clones in Library**
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMVEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMVEC) – bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMVEC) – VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient	303467

Library (Lib#)	Description	Number of Clones in Library
	(MICRODISSECTED PCR (OligodT) cDNA library)	
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23-	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349

The KM12L4 cell line is derived from the KM12C cell line (Morikawa, et al., *Cancer Research* (1988) *48*:6863). The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B_2 surgical specimen (Morikawa *et al. Cancer Res.* (1988) *48*:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman *et al. Nucl. Acids. Res.* (1995) *23*:4007; Bao-Ling *et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) *21*:3269). The KM12C and KM12C-derived cell lines (*e.g.*, KM12L4, KM12L4-A, *etc.*) are well-recognized in the art as a model cell line for the study of colon cancer (see, *e.g.*, Moriakawa *et al.*, *supra*; Radinsky *et al. Clin. Cancer Res.* (1995) *1*:19; Yeatman *et al.*, (1995) *supra*; Yeatman *et al. Clin. Exp. Metastasis* (1996) *14*:246). The MDA-MB-231 cell line (Brinkley et al. *Cancer Res.* (1980) *40*:3118-3129) was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) *53*:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, *e.g.*, Chandrasekaran *et al.*, *Cancer Res.* (1979) *39*:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) *41*:4965 (MDA-

MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) *77*:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) *26*:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) *40*:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) *11*:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) *10*:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) *15*:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) *8*:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cells were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz cells were derived from normal prostate epithelium. The WOca cells are Gleason Grade 4 cell line.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) *37*(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the

second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5 , where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974). .

Using this approach, a number of polynucleotide sequences were identified as being differentially expressed between, for example, cells derived from high metastatic potential cancer tissue and low metastatic cancer cells, and between cells derived from metastatic cancer tissue and normal tissue. Evaluation of the levels of expression of the genes corresponding to these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes corresponding to differentially expressed sequences described herein can be therapeutic targets due to their involvement in regulation (*e.g.*, inhibition or promotion) of development of, for example, the metastatic phenotype. For example, sequences that correspond to genes that are increased in expression in high metastatic potential cells relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

Detection of the relative expression levels of differentially expressed polynucleotides described herein can provide valuable information to guide the clinician in the choice of therapy. For example, a patient sample exhibiting an expression level of one or more of these polynucleotides that corresponds to a gene that is increased in expression in metastatic or high metastatic potential cells may warrant more aggressive treatment for the patient. In contrast, detection of expression levels of a polynucleotide sequence that corresponds to expression levels associated with that of low metastatic potential cells may warrant a more positive prognosis than

the gross pathology would suggest.

The differential expression of the polynucleotides described herein can thus be used as, for example, diagnostic markers, prognostic markers, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The differential expression data for polynucleotides of the invention that have been identified as being differentially expressed across various combinations of the libraries described above is summarized in Table 4 (inserted prior to the claims). Table 4 provides: 1) the Sequence Identification Number ("SEQ ID") assigned to the polynucleotide; 2) the cluster ("CLUST") to which the polynucleotide has been assigned as described above; 3) the library comparisons that resulted in identifcation of the polynucleotide as being differentially expressed ("PairAB-text"), with shorthand names of the compared libraries provided in parentheses following the library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("B"); 6) the "RATIO PLUS" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "RATIO MINUS" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

Example 4: Differential Expression of a Polynucleotides Associated with Metastatic Potential in Breast Cancer

Differential expression was examined in breast cancer cells having either high metastatic potential or low metastatic potential. A single cluster, Cluster Identification No. 10154, was identified as displaying low expression in the high metastatic potential breast cancer cells (Library 3), and significantly increased expression – approximately 100-fold higher -- in the low metastatic potential cells (Library 4). Specifically, three clones were identified that were expressed in Library 3, the high metastatic potential breast cancer library, while 317 clones were expressed in Library 4, the low metastatic potential breast cancer library. The two sequences assigned to this particular cluster, SEQ ID NO:315 and SEQ ID NO:316, both displayed this differential expression, suggesting that the two sequences are likely associated with a single transcript.

SEQ ID NO:315 and SEQ ID NO:316 were then used as query sequences to search for homologous sequences in GenBank as described in Examples 1 and 2. SEQ ID NO: 315 displayed identity to the GenBank entry H72034 (SEQ ID NO:317) and SEQ ID NO:316 displayed identity to GenBank entry AA707002 (SEQ ID NO:318). SEQ ID NO:315 displays striking identity to the 3' end of SEQ ID NO:317 (See Figures 1A and 1B), while SEQ ID NO:316 displays striking identity to the 5' end of SEQ ID NO:318 (See Figure 2). Clones of H72034 and AA707002 were ordered

from the I.M.A.G.E. Consortium at the Lawrence Livermore National Laboratories (Livermore, California) for further studies.

Restriction Mapping of Clones H72034 and AA707002

The newly identified sequences were digested with a number of different restriction endonucleases to construct a restriction map of each of the clones. An appropriate amount of each clone, SEQ ID NO:317 or SEQ ID NO:318, was digested with various enzymes, and the restriction fragments identified as follows:

SEQ ID NO:317

Enzyme	#Cuts	Positions							
AluI	5	331	1029	1422	1595	1977			
BamHI	2	1836	2089						
BstEII	1	936							
BstXI	1	1033							
HaeIII	12	145	300	453	497	582	780		
		1102	1536	1561	1722	1981	2062		
HinfI	12	5	154	205	325	397	473	610	820
968			1295	1426	2066				
KpnI	1	1938							
MspI	6	78	739	1098	2038	2077	2093		
NcoI	2	2013	2058						
PstI	1	1501							
PvuII	2	331	1422						
Sau3AI	6	1270	1813	1819	1836	1894	2089		
SphI	1	1870							
XhoI	1	1413							

SEQ ID NO:318

Enzyme	#Cuts	Positions							
AluI	9	19	245	367	553	586	874	904	996
1214									
BamHI	1	407							
BglI	1	1056							
BglII	1	475							
BstEI	1	1108							
HaeIII	10	153	348	485	867	518	628	780	867
915			1016	1312					
HindIII	2	243	872						
HinfI	1	1353							
KpnI	1	132							
MspI	2	1196	1261						
PstI	1	823							
PvuII	1	996							
Sau3AI	7	66	407	475	504	750	850	1024	

The restriction maps based on the identified sites can be used to determine the position of each clone relative to the genomic sequences, and to confirm the 5'-3'orientation of the clones.

Amplification and Purification of Transcript

A transcript in this region upregulated in low metastatic cancers which contain sequences from SEQ ID NOS: 315-318 is identified using a technique such as polymerase chain reaction (PCR) amplification. Based on the sequences identified and the original sequences of the cluster, primers can be designed to isolate the full length cDNA from a library constructed from the breast cancer cell line with low metastatic potential.

A cDNA template for use in the amplification reaction is generated from total RNA isolated from the high metastatic breast cell line. RNA is reverse transcribed using oligo-dT primer to generate first strand cDNA. cDNA is synthesized by denaturing 3µl of total RNA, 2 µl oligo-dT primer at 20 µM, and 5 µl DEPC water for 8 minutes at 65°C followed by reverse transcription at 52°C for 1 hour in a reaction containing the denatured RNA/primer plus 4µl 1 5X cDNA buffer (GibcoBRL), 1 µl 0.1 M dithiothreitol, 1 µl 40 U/ l RNAseOUT (GibcoBRL), 1 µl DEPC water, 2 µl 10 mM dNTP (GibdoBRL), and 1 µl 15 U/ l Thermoscript reverse transcriptase (GibcoBRL). The reaction was terminated by a 5-min incubation at 85°C, and the RNA was removed by 1 µl 2 U/ l RNAse H at 37°C for thirty minutes.

Based on the determined orientation of the clones, primers are designed to amplify a full-length clone corresponding to the differentially expressed transcript in this region. Forward primers that are used to amplify the full-length clone are taken from the 5' end of SEQ ID NO:17 as follows:

F1 5'- TGGGATATAGTCTCGTGGTGCG -3' (SEQ ID NO:319)
F2 5'- TGATTCGATGTCATCAGTCCCG-3' (SEQ ID NO:320)

Primer F1 is taken from residues 51-62 of SEQ ID NO: 317, and primer F2 is taken from residues 212-233 Of SEQ ID NO:17. Both forward primers are near the 5' end of this sequence.

Reverse Primers are designed using sequences complementary to the 3' end of clone 10154-3 as follows:

R1 5'- TGTGTCACAGCCAGACATGAGC (SEQ ID NO:321)
R2 5' – TGCAAACATACACAGGGACCG (SEQ ID NO:322)

Primer R1 is based on residues 573-552 of SEQ ID NO:318, and R2 is based on residues 399-379 of SEQ ID NO:318.

PCR is performed using a 5μl aliquot of the first strand cDNA synthesis reaction, and a primer pair, e.g., F1 and R1, F1 and R2, F2 and R1, or F2 and R2. An open reading frame is amplified using 2 μl of the reverse transcription product as template in a PCR reaction containing 5 μl of 10x PCR buffer (GibcoBRL), 1 μl 50 mM Mg_2SO_4, 1 μl 10 mM dNTP, 1 μl F1 or F2 primer, 1 μl R1 primer, 2.5 U High Fidelity Platinum Taq DNA polymerase (GibcoBRL), and water to 50 μl. The molecule is amplified using 30 rounds of amplification in a thermal cycler at the following temperatures: 1 minute at 95°C; 1 minute at 55°C and 2 minutes at 72°C. The 30 cycles was followed by a 10 minute extension at 72°C.

Following amplification of the sequences, the PCR products are loaded on a 1% TEA gel and subjected to gel purification. One or more bands can be isolated from the gel and the DNA was purified using a QIAquick® Gel Extraction Kit (Qiagen, Valencia, CA). The purified fragment was cloned into a bacterial vector and transformed into the bacterial strain DH5α. Following cloning of the purified fragment(s), the DNA can be isolated and sequenced to confirm that a band corresponds to a transcript from this genetic region.

The reactions are carried out with two different 5' and 3' primers to increase the likelihood that the reaction will yield an amplification product. Other primers may also be designed from the predicted 5' and/or 3' end of the sequence, as will be apparent to one skilled in the art upon reading this disclosure, and thus other primers may be designed from the general region of SEQ ID NOS:317 and 318 that may yield better results than the disclosed primers.

In order to obtain additional sequences 5' to the end of a partial cDNA, 5' rapid amplification of cDNA ends (RACE) can be performed to ensure that the entire transcript has been identified. See *PCR Protocols: A Guide to Methods and Applications,* (1990) Academic Press, Inc. Following isolation of a cDNA using the F1-R1 or F2-R1 primer pairs, additional primers can be designed to perform RACE. The primers can be designed from the sequence of 10154-1 as follows:

5'-TTTAGCAGCACTAATGACTGTGGC-3' (SEQ ID NO:323)
5'-CGCCGTGAATTACTGTGGATGG-3' (SEQ ID NO:324)

The two RACE primers are designed based residues 286-263 and 396-375 of SEQ ID NO:317, respectively.

These sequences can be used to obtain any transcript sequences 5' to the amplification products obtained using the PCR protocol described above.

Northern Analysis

Other techniques can be used for confirming differential expression of the full-length transcript. For example, a Northern Blot can be used to verify differential expression of SEQ ID

NOS:317 and 318 in a breast cancer cells with low metastatic potential compared to breast cancer cells with high metastatic potential. Northern analysis can be accomplished by methods well-known in the art. Briefly, RNA is individually isolated from breast cancer cells having high metastatic potential and breast cancer cells having low metastatic potential, *e.g.,* a product such as RNeasy Mini Kits (Qiagen, CA) or NucleoSpin® RNA II Kit (Clontech, Palo Alto, CA). The isolated RNA samples are For Northern analysis, RNA isolated from the cells was electrophoresed on a denaturing formaldehyde agarose gel and transferred onto a membrane such as a supported nitrocellulose membrane (Schleicher & Schuell).

Rapid-Hyb buffer (Amersham Life Science, Little Chalfont, England) with 5 mg/ml denatured single stranded sperm DNA is pre-warmed to 65°C and the RNA blots are pre-hybridized in the buffer with shaking at 65°C for 30 minutes. Gene-specific DNA probes (50 ng per reaction) labeled with [α-^{32}P]dCTP (3000Ci/mmol, Amersham Pharmacia Biotech Inc., Piscataway, NJ) (Prime-It RmT Kit, Stratagene, La Jolla, CA) and purified with ProbeQuant^{TM} G-50 Micro Columns (Amersham Pharmacia Biotech Inc.) are added and hybridized to the blots with shaking at 65°C for overnight. The blots are washed in 2x SSC, 0.1%(w/v) SDS at room temperature for 20 minutes, twice in 1x SSC, 0.1%(w/v) SDS at 65°C for 15 minutes, then exposed to Hyperfilms (Amersham Life Science).

<u>Example 6: Identification of Differentially Expressed Genes by Array Analysis with Patient Tissue Samples</u>

Differentially expressed genes corresponding to the polynucleotides described herein were also identified by microarray hybridization analysis using materials obtained from patient tissue samples. The biological materials used in these experiments are described below.

<u>Source of patient tissue samples</u>

Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, *e.g.*, Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001). Table 8 (inserted following the last page of the Examples) provides information about each patient from which the samples were isolated, including: the Patient ID and Path ReportID, numbers assigned to the patient and the pathology reports for identification purposes; the anatomical location of the tumor (AnatomicalLoc); The Primary Tumor Size; the Primary Tumor Grade; the Histopathologic Grade; a description of local sites to which the tumor had invaded (Local Invasion); the presence of lymph node metastases (Lymph Node Metastasis); incidence of lymph node metastases (provided as number of lymph nodes positive for metastasis over the number of lymph nodes examined)

(Incidence Lymphnode Metastasis); the Regional Lymphnode Grade; the identification or detection of metastases to sites distant to the tumor and their location (Distant Met & Loc);a description of the distant metastases (Description Distant Met); the grade of distant metastasis (Distant Met Grade); and general comments about the patient or the tumor (Comments). Adenoma was not described in any of the patients. ; adenoma dysplasia (described as hyperplasia by the pathologist) was described in Patient ID No. 695. Extranodal extensions were described in two patients, Patient ID Nos. 784 and 791. Lymphovascular invasion was described in seven patients, Patient ID Nos. 128, 278, 517, 534, 784, 786, and 791.. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Source of polynucleotides on arrays

Polynucleotides on arrays

Polynucleotides spotted on the arrays were generated by PCR amplification of clones derived from cDNA libraries. The clones used for amplification were either the clones from which the sequences described herein (SEQ ID NOS:1-316) were derived, or are clones having inserts with significant polynucleotide sequence overlap with the sequences described herein (SEQ ID NO:1-316) as determined by BLAST2 homology searching.

Microarray Design

Each array used in the examples below had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides.

The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1 . For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

Microarray analysis

cDNA probes were prepared from total RNA isolated from the patient cells described in above (Table 8). Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in*

vitro to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling. Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red).

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. For initial analysis of the microarrays, the hypothesis was accepted if $p>10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p>0.05$).

Table 9 below summarize the results of the differential expression analysis. Each table provides: the SEQ ID NO of the polynucleotide corresponding to the polynucleotide on the spot on the array; the Spot ID (an identifier assigned to the spot so as to distinguish it from spots on the same and different arrays), the number of patients for whom there was information obtained from the array (Num Ratios), and the percentage of patients in which expression was detected at greater than or equal to a two-fold increase (>=2x), greater than or equal to a five-fold increase (>=5x), or less than or equal to a 1/2 -fold decrease (<=halfx) relative to matched normal control tissue.

In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at least one sample and the ratio value is greater than at least about 1.2 fold, preferably greater than at least about 1.5 fold , more preferably greater than at least about 2 fold, where the ratio value is calculated using the method described above.

A differential expression ratio of 1 indicates that the expression level of the gene in the tumor cell was not statistically different from expression of that gene in normal colon cells of the same patient. A differential expression ratio significantly greater than 1 in cancerous colon cells relative to normal colon cells indicates that the gene is increased in expression in cancerous cells relative to normal cells, indicating that the gene plays a role in the development of the cancerous phenotype, and may be involved in promoting metastasis of the cell. Detection of gene products from such genes can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target.

Likewise, a differential expression ratio significantly less than 1 in cancerous colon cells relative to normal colon cells indicates that, for example, the gene is involved in suppression of the cancerous phenotype. Increasing activity of the gene product encoded by such a gene, or replacing such activity, can provide the basis for chemotherapy. Such gene can also serve as markers of

cancerous cells, e.g., the absence or decreased presence of the gene product in a colon cell relative to a normal colon cell indicates that the cell may be cancerous.

Table 9.

SEQ ID NO:	SpotID	Num Ratios	>=2x	>=5x	<=halfx
8	579	33	87.88	39.39	3.03
12	22300	33	33.33	18.18	6.06
26	21886	33	33.33	0.00	3.03
64	9487	33	33.33	12.12	3.03
248	28179	28	32.14	0.00	0.00
253	28179	28	32.14	0.00	0.00
272	28179	28	32.14	0.00	0.00
292	9111	33	33.33	18.18	3.03
295	19980	33	33.33	6.06	0.00
309	23993	33	42.42	3.03	3.03

Deposit Information. The following materials were deposited with the American Type Culture Collection (CMCC = Chiron Master Culture Collection).

Table 5. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 6 below provides the ATCC Accession Nos. of the ES deposits, all of which were deposited on or before May 13, 1999. The names of the clones contained within each of these deposits are provided in the Table 7 (inserted before the claims).

Table 6: Pools of Clones and Libraries Deposited with ATCC on or before March 28, 2000

Cell Line	CMCC	ATCC
ES75	5140	PTA-1102
ES76	5141	PTA-1103
ES77	5142	PTA-1104
ES78	5143	PTA-1105
ES79	5144	PTA-1106
ES80	5145	PTA-1107
ES81	5146	PTA-1108
ES82	5147	PTA-1109
ES83	5148	PTA-1110
ES84	5149	PTA-1111

The deposits described herein are provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
1	819545	RTA22200265F.k.06.1.P.Seq	F	M00064554D:A03	CH22PRC
2	377944	RTA22200251F.j.02.1.P.Seq	F	M00063482A:A08	CH21PRN
3	818497	RTA22200252F.a.13.1.P.Seq	F	M00063514C:D03	CH21PRN
4	819498	RTA22200252F.n.05.1.P.Seq	F	M00063638C:G12	CH21PRN
5	455465	RTA22200264F.e.16.1.P.Seq	F	M00064454A:H10	CH22PRC
6	819069	RTA22200255F.f.01.1.P.Seq	F	M00063940D:F09	CH21PRN
7	672003	RTA22200265F.b.09.1.P.Seq	F	M00064517C:F11	CH22PRC
8	728115	RTA22200253F.o.24.1.P.Seq	F	M00063838B:G08	CH21PRN
9	372700	RTA22200260F.b.20.1.P.Seq	F	M00063580C:A06	CH22PRC
10	818056	RTA22200266F.c.13.1.P.Seq	F	M00064593D:C01	CH22PRC
11	818497	RTA22200255F.a.17.1.P.Seq	F	M00063920D:H02	CH21PRN
12	729832	RTA22200267F.l.21.1.P.Seq	F	M00064714A:G03	CH22PRC
13	505514	RTA22200251F.b.21.1.P.Seq	F	M00063158A:A01	CH21PRN
14	376488	RTA22200254F.c.05.1.P.Seq	F	M00063852B:D08	CH21PRN
15	376488	RTA22200260F.b.09.1.P.Seq	F	M00063578C:A06	CH22PRC
16	748572	RTA22200254F.c.07.1.P.Seq	F	M00063852D:F07	CH21PRN
17	549934	RTA22200253F.k.18.1.P.Seq	F	M00063801B:D04	CH21PRN
18	819069	RTA22200255F.e.24.1.P.Seq	F	M00063940D:F09	CH21PRN
19	817618	RTA22200253F.n.16.1.P.Seq	F	M00063828D:E05	CH21PRN
20	124396	RTA22200263F.a.11.2.P.Seq	F	M00064375B:G07	CH22PRC
21	404375	RTA22200260F.m.08.1.P.Seq	F	M00063967D:G02	CH22PRC
22	391820	RTA22200261F.f.02.1.P.Seq	F	M00064000B:C03	CH22PRC
23	672003	RTA22200267F.i.06.1.P.Seq	F	M00064693D:F08	CH22PRC
24	830620	RTA22200263F.n.09.1.P.Seq	F	M00064424B:C12	CH22PRC
25	450399	RTA22200251F.f.23.1.P.Seq	F	M00063467D:H07	CH21PRN
26	450982	RTA22200261F.n.18.1.P.Seq	F	M00064307B:G02	CH22PRC
27	819894	RTA22200264F.h.18.1.P.Seq	F	M00064467B:D06	CH22PRC
28	379302	RTA22200257F.j.02.3.P.Seq	F	M00064178C:C04	CH21PRN
29	379746	RTA22200256F.e.16.1.P.Seq	F	M00064086C:E01	CH21PRN
30	124863	RTA22200265F.m.06.1.P.Seq	F	M00064564A:C02	CH22PRC
31	379154	RTA22200257F.c.11.1.P.Seq	F	M00064151B:C07	CH21PRN
32	830620	RTA22200262F.l.23.1.P.Seq	F	M00064358C:D09	CH22PRC
33	389409	RTA22200266F.l.24.1.P.Seq	F	M00064631A:C07	CH22PRC
34	397284	RTA22200262F.i.22.1.P.Seq	F	M00064346C:B09	CH22PRC
35	819440	RTA22200264F.e.19.1.P.Seq	F	M00064454C:B06	CH22PRC
36	389409	RTA22200266F.m.01.1.P.Seq	F	M00064631A:C07	CH22PRC
37	518848	RTA22200265F.n.15.1.P.Seq	F	M00064571C:C04	CH22PRC
38	830620	RTA22200263F.a.21.1.P.Seq	F	M00064376A:A05	CH22PRC
39	379154	RTA22200256F.f.20.1.P.Seq	F	M00064090D:D09	CH21PRN
40	818544	RTA22200256F.h.04.1.P.Seq	F	M00064105B:A03	CH21PRN
41	817375	RTA22200251F.a.15.1.P.Seq	F	M00063152C:B07	CH21PRN

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
42	455264	RTA22200259F.e.23.1.P.Seq	F	M00063539C:C11	CH22PRC
43	817503	RTA22200266F.k.11.1.P.Seq	F	M00064624D:C09	CH22PRC
44	377696	RTA22200256F.d.21.1.P.Seq	F	M00064082D:D10	CH21PRN
45	375596	RTA22200261F.h.10.1.P.Seq	F	M00064009A:C01	CH22PRC
46	817689	RTA22200263F.h.05.1.P.Seq	F	M00064399A:E01	CH22PRC
47	831867	RTA22200262F.i.15.2.P.Seq	F	M00064345A:A03	CH22PRC
48	830085	RTA22200261F.k.14.1.P.Seq	F	M00064293D:B12	CH22PRC
49	389627	RTA22200264F.c.10.1.P.Seq	F	M00064447B:C06	CH22PRC
50	397284	RTA22200259F.k.09.1.P.Seq	F	M00063555B:D01	CH22PRC
51	380063	RTA22200261F.j.02.1.P.Seq	F	M00064014D:H05	CH22PRC
52	830931	RTA22200266F.m.23.1.P.Seq	F	M00064633C:A03	CH22PRC
53	819321	RTA22200257F.1.03.3.P.Seq	F	M00064194C:D02	CH21PRN
54	475587	RTA22200261F.c.01.1.P.Seq	F	M00063990A:D05	CH22PRC
55	819046	RTA22200255F.a.18.1.P.Seq	F	M00063920D:H05	CH21PRN
56	817477	RTA22200253F.g.21.1.P.Seq	F	M00063784A:H12	CH21PRN
57	475587	RTA22200261F.b.24.1.P.Seq	F	M00063990A:D05	CH22PRC
58	728115	RTA22200253F.p.01.1.P.Seq	F	M00063838B:G08	CH21PRN
59	389627	RTA22200260F.i.24.1.P.Seq	F	M00063957A:E02	CH22PRC
60	403453	RTA22200256F.i.24.1.P.Seq	F	M00064113B:C04	CH21PRN
61	508525	RTA22200255F.d.10.1.P.Seq	F	M00063931B:F07	CH21PRN
62	819525	RTA22200261F.n.20.1.P.Seq	F	M00064307C:G03	CH22PRC
63	817618	RTA22200255F.i.03.1.P.Seq	F	M00064025D:H12	CH21PRN
64	819403	RTA22200254F.h.14.1.P.Seq	F	M00063888D:D05	CH21PRN
65	553242	RTA22200254F.g.20.1.P.Seq	F	M00063886A:B06	CH21PRN
66	817417	RTA22200255F.a.10.1.P.Seq	F	M00063919C:E07	CH21PRN
67	817618	RTA22200252F.f.13.1.P.Seq	F	M00063604A:B11	CH21PRN
68	611440	RTA22200262F.e.04.2.P.Seq	F	M00064328B:H09	CH22PRC
69	817375	RTA22200260F.m.06.1.P.Seq	F	M00063967C:A12	CH22PRC
70	213577	RTA22200255F.i.23.1.P.Seq	F	M00064033C:C11	CH21PRN
71	820061	RTA22200265F.p.10.1.P.Seq	F	M00064579D:E11	CH22PRC
72	455264	RTA22200259F.m.06.1.P.Seq	F	M00063559D:G03	CH22PRC
73	455264	RTA22200255F.o.23.1.P.Seq	F	M00064059A:C11	CH21PRN
74	380331	RTA22200255F.b.19.1.P.Seq	F	M00063926A:H04	CH21PRN
75	380331	RTA22200252F.b.19.1.P.Seq	F	M00063518D:A01	CH21PRN
76	817455	RTA22200267F.o.01.1.P.Seq	F	M00064723D:H03	CH22PRC
77	423967	RTA22200252F.a.20.1.P.Seq	F	M00063515B:H02	CH21PRN
78	220584	RTA22200261F.m.14.1.P.Seq	F	M00064302A:D10	CH22PRC
79	817688	RTA22200251F.e.20.1.P.Seq	F	M00063462D:D07	CH21PRN
80	549934	RTA22200253F.n.10.1.P.Seq	F	M00063826A:D03	CH21PRN
81	819149	RTA22200255F.e.16.1.P.Seq	F	M00063938B:H07	CH21PRN
82	817455	RTA22200267F.n.24.1.P.Seq	F	M00064723D:H03	CH22PRC

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
83	377696	RTA22200251F.j.03.1.P.Seq	F	M00063482A:F07	CH21PRN
84	830146	RTA22200260F.b.07.1.P.Seq	F	M00063578B:E02	CH22PRC
85	194490	RTA22200264F.l.07.1.P.Seq	F	M00064481C:F03	CH22PRC
86	819460	RTA22200257F.m.15.3.P.Seq	F	M00064200D:E08	CH21PRN
87	819018	RTA22200257F.p.01.3.P.Seq	F	M00064212D:E04	CH21PRN
88	830620	RTA22200259F.p.24.1.P.Seq	F	M00063571B:G03	CH22PRC
89	141079	RTA22200262F.k.19.1.P.Seq	F	M00064354A:A10	CH22PRC
90	376588	RTA22200256F.e.04.1.P.Seq	F	M00064083D:E05	CH21PRN
91	380604	RTA22200264F.g.05.1.P.Seq	F	M00064460C:B01	CH22PRC
92	413138	RTA22200260F.b.05.1.P.Seq	F	M00063577C:C02	CH22PRC
93	818544	RTA22200265F.e.12.1.P.Seq	F	M00064527A:H07	CH22PRC
94	647435	RTA22200257F.h.08.1.P.Seq	F	M00064172C:A02	CH21PRN
95	551785	RTA22200266F.c.09.1.P.Seq	F	M00064593A:A05	CH22PRC
96	17092	RTA22200261F.f.17.1.P.Seq	F	M00064002C:F06	CH22PRC
97	818326	RTA22200251F.i.06.1.P.Seq	F	M00063478C:D01	CH21PRN
98	377944	RTA22200262F.e.03.2.P.Seq	F	M00064328B:H04	CH22PRC
99	745559	RTA22200262F.m.04.1.P.Seq	F	M00064359B:H12	CH22PRC
100	818326	RTA22200265F.d.08.1.P.Seq	F	M00064524A:A09	CH22PRC
101	379879	RTA22200264F.b.23.1.P.Seq	F	M00064446A:D11	CH22PRC
102	819640	RTA22200257F.f.24.1.P.Seq	F	M00064165A:B12	CH21PRN
103	818326	RTA22200265F.a.14.1.P.Seq	F	M00064514D:F11	CH22PRC
104	243524	RTA22200265F.g.04.1.P.Seq	F	M00064532D:G06	CH22PRC
105	43995	RTA22200261F.l.02.1.P.Seq	F	M00064294D:F01	CH22PRC
106	597854	RTA22200262F.g.06.2.P.Seq	F	M00064337D:F01	CH22PRC
107	268290	RTA22200260F.p.14.1.P.Seq	F	M00063981D:A06	CH22PRC
108	818043	RTA22200256F.p.10.2.P.Seq	F	M00064138A:F11	CH21PRN
109	830930	RTA22200267F.b.03.1.P.Seq	F	M00064652B:D09	CH22PRC
110	389627	RTA22200260F.j.01.1.P.Seq	F	M00063957A:E02	CH22PRC
111	378730	RTA22200260F.i.07.1.P.Seq	F	M00063955C:F07	CH22PRC
112	819037	RTA22200260F.n.09.1.P.Seq	F	M00063972C:E10	CH22PRC
113	830397	RTA22200261F.g.14.1.P.Seq	F	M00064005D:A08	CH22PRC
114	450247	RTA22200261F.e.10.1.P.Seq	F	M00063998C:E09	CH22PRC
115	819273	RTA22200252F.b.09.1.P.Seq	F	M00063517A:A04	CH21PRN
116	587779	RTA22200257F.i.11.3.P.Seq	F	M00064175B:B09	CH21PRN
117	818639	RTA22200256F.j.09.1.P.Seq	F	M00064115B:E12	CH21PRN
118	615617	RTA22200261F.o.13.1.P.Seq	F	M00064309C:H09	CH22PRC
119	79309	RTA22200257F.j.13.3.P.Seq	F	M00064180A:G03	CH21PRN
120	748994	RTA22200261F.o.20.1.P.Seq	F	M00064310C:A10	CH22PRC
121	818682	RTA22200258F.h.07.1.P.Seq	F	M00064271B:D03	CH21PRN
122	373061	RTA22200253F.j.09.1.P.Seq	F	M00063795C:D09	CH21PRN
123	484413	RTA22200253F.g.09.1.P.Seq	F	M00063781B:B10	CH21PRN

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
124	819273	RTA22200258F.h.04.1.P.Seq	F	M00064270B:B03	CH21PRN
125	569532	RTA22200252F.h.18.1.P.Seq	F	M00063613D:C11	CH21PRN
126	170313	RTA22200255F.g.20.1.P.Seq	F	M00063949D:A05	CH21PRN
127	818682	RTA22200253F.p.14.1.P.Seq	F	M00063841A:B09	CH21PRN
128	377188	RTA22200255F.1.06.1.P.Seq	F	M00064043D:C09	CH21PRN
129	518848	RTA22200257F.j.22.3.P.Seq	F	M00064186C:B03	CH21PRN
130	45592	RTA22200259F.1.08.1.P.Seq	F	M00063557D:C07	CH22PRC
131	819273	RTA22200255F.n.19.1.P.Seq	F	M00064053C:G04	CH21PRN
132	397284	RTA22200251F.a.06.1.P.Seq	F	M00063151D:B10	CH21PRN
133	818326	RTA22200258F.e.14.1.P.Seq	F	M00064260C:E05	CH21PRN
134	819037	RTA22200251F.c.15.1.P.Seq	F	M00063452A:F08	CH21PRN
135	817417	RTA22200253F.m.14.1.P.Seq	F	M00063818C:A09	CH21PRN
136	819640	RTA22200254F.i.11.1.P.Seq	F	M00063891A:F11	CH21PRN
137	818771	RTA22200254F.i.19.1.P.Seq	F	M00063892B:G02	CH21PRN
138	389627	RTA22200254F.k.10.1.P.Seq	F	M00063898A:A10	CH21PRN
139	379067	RTA22200260F.e.20.1.P.Seq	F	M00063593A:D03	CH22PRC
140	818544	RTA22200251F.f.02.1.P.Seq	F	M00063463D:B05	CH21PRN
141	819440	RTA22200251F.j.22.1.P.Seq	F	M00063485A:E05	CH21PRN
142	817417	RTA22200251F.k.10.1.P.Seq	F	M00063487C:C02	CH21PRN
143	385307	RTA22200262F.k.11.1.P.Seq	F	M00064352C:H01	CH22PRC
144	611440	RTA22200263F.d.24.2.P.Seq	F	M00064386B:C02	CH22PRC
145	376056	RTA22200259F.e.16.1.P.Seq	F	M00063538D:B01	CH22PRC
146	611440	RTA22200263F.d.24.1.P.Seq	F	M00064386B:C02	CH22PRC
147	820061	RTA22200264F.f.09.1.P.Seq	F	M00064457D:C09	CH22PRC
148	617825	RTA22200264F.p.06.1.P.Seq	F	M00064508A:B09	CH22PRC
149	819440	RTA22200257F.h.17.1.P.Seq	F	M00064173B:E01	CH21PRN
150	819145	RTA22200266F.m.08.1.P.Seq	F	M00064631C:H11	CH22PRC
151	817653	RTA22200265F.p.07.1.P.Seq	F	M00064579A:C06	CH22PRC
152	611440	RTA22200263F.e.01.1.P.Seq	F	M00064386B:C02	CH22PRC
153	375958	RTA22200264F.j.22.1.P.Seq	F	M00064476D:C04	CH22PRC
154	611440	RTA22200257F.a.20.1.P.Seq	F	M00064144D:A07	CH21PRN
155	831049	RTA22200266F.o.13.1.P.Seq	F	M00064637B:F03	CH22PRC
156	818162	RTA22200266F.g.18.1.P.Seq	F	M00064610D:H01	CH22PRC
157	553200	RTA22200263F.p.02.1.P.Seq	F	M00064429D:B07	CH22PRC
158	139677	RTA22200254F.o.07.1.P.Seq	F	M00063910D:A12	CH21PRN
159	139677	RTA22200252F.c.11.1.P.Seq	F	M00063520D:E11	CH21PRN
160	397284	RTA22200262F.i.22.2.P.Seq	F	M00064346C:B09	CH22PRC
161	385810	RTA22200256F.m.04.2.P.Seq	F	M00064126C:F12	CH21PRN
162	404624	RTA22200261F.e.07.1.P.Seq	F	M00063997C:B12	CH22PRC
163	375958	RTA22200262F.b.14.2.P.Seq	F	M00064322C:A10	CH22PRC
164	616555	RTA22200265F.b.24.1.P.Seq	F	M00064520A:E04	CH22PRC

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
165	616555	RTA22200265F.c.01.1.P.Seq	F	M00064520A:E04	CH22PRC
166	295694	RTA22200260F.o.20.1.P.Seq	F	M00063978B:B06	CH22PRC
167	36113	RTA22200265F.e.06.1.P.Seq	F	M00064526D:F05	CH22PRC
168	831812	RTA22200263F.f.05.1.P.Seq	F	M00064390A:C05	CH22PRC
169	817653	RTA22200252F.g.23.1.P.Seq	F	M00063610D:C11	CH21PRN
170	397284	RTA22200252F.m.15.1.P.Seq	F	M00063636A:E01	CH21PRN
171	817979	RTA22200253F.p.15.1.P.Seq	F	M00063841A:E08	CH21PRN
172	817653	RTA22200255F.m.18.1.P.Seq	F	M00064048C:G12	CH21PRN
173	611440	RTA22200253F.f.03.1.P.Seq	F	M00063774A:D09	CH21PRN
174	386014	RTA22200261F.f.06.1.P.Seq	F	M00064001A:B03	CH22PRC
175	549981	RTA22200255F.b.10.1.P.Seq	F	M00063925B:F04	CH21PRN
176	193373	RTA22200255F.l.21.1.P.Seq	F	M00064046A:G02	CH21PRN
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179	36113	RTA22200255F.d.16.1.P.Seq	F	M00063932D:G08	CH21PRN
180	817503	RTA22200253F.l.16.1.P.Seq	F	M00063805D:E05	CH21PRN
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182	141079	RTA22200252F.f.23.1.P.Seq	F	M00063606C:B04	CH21PRN
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188	830930	RTA22200264F.e.10.1.P.Seq	F	M00064452D:E11	CH22PRC
189	818497	RTA22200256F.d.07.1.P.Seq	F	M00064079C:A10	CH21PRN
190	373928	RTA22200256F.d.19.1.P.Seq	F	M00064082A:A08	CH21PRN
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193	730318	RTA22200264F.c.09.1.P.Seq	F	M00064447B:A07	CH22PRC
194	44183	RTA22200271F.a.01.1.P.Seq	F	M00021929A:D03	CH03MAH
195	373928	RTA22200255F.d.22.1.P.Seq	F	M00063934B:E04	CH21PRN
196	404624	RTA22200255F.d.23.1.P.Seq	F	M00063934C:C10	CH21PRN
197	403173	RTA22200253F.a.21.1.P.Seq	F	M00063685A:C02	CH21PRN
198	372700	RTA22200253F.c.06.1.P.Seq	F	M00063689D:E12	CH21PRN
199	374343	RTA22200261F.h.04.1.P.Seq	F	M00064008A:B01	CH22PRC
200	597854	RTA22200255F.j.03.1.P.Seq	F	M00064033D:B01	CH21PRN
201	817417	RTA22200255F.a.23.1.P.Seq	F	M00063922B:A12	CH21PRN
202	818497	RTA22200257F.k.05.3.P.Seq	F	M00064188B:G08	CH21PRN
203	377696	RTA22200255F.f.15.1.P.Seq	F	M00063943B:G12	CH21PRN
204	379105	RTA22200252F.n.19.1.P.Seq	F	M00063642B:A08	CH21PRN
205	831188	RTA22200267F.o.02.1.P.Seq	F	M00064723D:H11	CH22PRC

Table 1

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208	376056	RTA22200254F.i.03.1.P.Seq	F	M00063890A:F11	CH21PRN
209	831812	RTA22200266F.j.10.1.P.Seq	F	M00064620C:D01	CH22PRC
210	141079	RTA22200260F.i.14.1.P.Seq	F	M00063956A:F05	CH22PRC
211	19148	RTA22200265F.o.18.1.P.Seq	F	M00064577C:B12	CH22PRC
212	124396	RTA22200252F.a.14.1.P.Seq	F	M00063514C:E08	CH21PRN
213	831026	RTA22200265F.c.03.1.P.Seq	F	M00064520A:F08	CH22PRC
214	819037	RTA22200263F.i.23.1.P.Seq	F	M00064405B:C04	CH22PRC
215	380207	RTA22200263F.i.19.1.P.Seq	F	M00064404C:G05	CH22PRC
216	819460	RTA22200255F.c.13.1.P.Seq	F	M00063928A:G09	CH21PRN
217	379067	RTA22200253F.g.23.1.P.Seq	F	M00063784C:E10	CH21PRN
218	403173	RTA22200252F.p.23.1.P.Seq	F	M00063682A:C04	CH21PRN
219	3856	RTA22200269F.a.05.1.P.Seq	F	M00003773D:H02	CH01COH
220	378551	RTA22200263F.d.17.1.P.Seq	F	M00064385D:C11	CH22PRC
221	456089	RTA22200272F.a.09.1.P.Seq	F	M00043134A:A05	CH19COP
222	549981	RTA22200267F.a.22.1.P.Seq	F	M00064650B:B07	CH22PRC
223	378551	RTA22200265F.m.21.1.P.Seq	F	M00064568A:H06	CH22PRC
224	819201	RTA22200256F.n.23.2.P.Seq	F	M00064132B:B07	CH21PRN
225	374826	RTA22200251F.c.20.1.P.Seq	F	M00063453B:F08	CH21PRN
226	389409	RTA22200253F.l.23.1.P.Seq	F	M00063807A:D12	CH21PRN
227	819149	RTA22200260F.a.17.1.P.Seq	F	M00063575B:G02	CH22PRC
228	389409	RTA22200255F.e.18.1.P.Seq	F	M00063939C:D06	CH21PRN
229	818165	RTA22200254F.h.15.1.P.Seq	F	M00063888D:F02	CH21PRN
230	817757	RTA22200252F.i.15.1.P.Seq	F	M00063617D:F09	CH21PRN
231	553242	RTA22200263F.i.20.1.P.Seq	F	M00064404D:A06	CH22PRC
232	385615	RTA22200265F.b.08.1.P.Seq	F	M00064517B:F10	CH22PRC
233	819102	RTA22200258F.h.19.1.P.Seq	F	M00064272C:G01	CH21PRN
234	817757	RTA22200255F.o.16.1.P.Seq	F	M00064057C:H10	CH21PRN
235	385615	RTA22200265F.b.07.1.P.Seq	F	M00064517B:F04	CH22PRC
236	385615	RTA22200253F.l.06.1.P.Seq	F	M00063804C:A11	CH21PRN
237	827355	RTA22200266F.n.23.1.P.Seq	F	M00064636B:A04	CH22PRC
238	817629	RTA22200259F.a.13.1.P.Seq	F	M00063165A:C09	CH22PRC
239	817514	RTA22200260F.h.02.1.P.Seq	F	M00063600C:C09	CH22PRC
240	817514	RTA22200252F.p.21.1.P.Seq	F	M00063681B:C02	CH21PRN
241	680563	RTA22200265F.f.13.1.P.Seq	F	M00064530B:H02	CH22PRC
242	827355	RTA22200255F.e.20.1.P.Seq	F	M00063939C:H01	CH21PRN
243	377286	RTA22200254F.a.04.1.P.Seq	F	M00063843B:D07	CH21PRN
244	680563	RTA22200258F.g.18.1.P.Seq	F	M00064268D:G03	CH21PRN
245	819156	RTA22200255F.h.06.1.P.Seq	F	M00064021D:H01	CH21PRN
246	220584	RTA22200261F.f.22.1.P.Seq	F	M00064003B:C10	CH22PRC

Table 1

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249	817508	RTA22200257F.h.01.1.P.Seq	F	M00064171D:E05	CH21PRN
250	817690	RTA22200257F.e.05.1.P.Seq	F	M00064159A:H03	CH21PRN
251	819156	RTA22200256F.h.13.1.P.Seq	F	M00064106C:G03	CH21PRN
252	830904	RTA22200266F.j.12.1.P.Seq	F	M00064620D:G05	CH22PRC
253	819498	RTA22200253F.b.04.1.P.Seq	F	M00063686B:E07	CH21PRN
254	817508	RTA22200257F.g.24.1.P.Seq	F	M00064171D:E05	CH21PRN
255	817508	RTA22200252F.a.19.1.P.Seq	F	M00063515B:F06	CH21PRN
256	831160	RTA22200267F.h.01.1.P.Seq	F	M00064690A:C04	CH22PRC
257	817762	RTA22200252F.k.13.1.P.Seq	F	M00063627C:F06	CH21PRN
258	377286	RTA22200266F.k.07.1.P.Seq	F	M00064624C:B03	CH22PRC
259	831160	RTA22200267F.g.24.1.P.Seq	F	M00064690A:C04	CH22PRC
260	819994	RTA22200256F.k.11.1.P.Seq	F	M00064119C:D12	CH21PRN
261	819994	RTA22200256F.k.09.1.P.Seq	F	M00064119B:H10	CH21PRN
262	373298	RTA22200259F.c.19.1.P.Seq	F	M00063533A:C12	CH22PRC
263	819894	RTA22200256F.m.03.2.P.Seq	F	M00064126C:C02	CH21PRN
264	372718	RTA22200260F.b.22.1.P.Seq	F	M00063580D:B06	CH22PRC
265	827355	RTA22200262F.l.20.1.P.Seq	F	M00064358A:G03	CH22PRC
266	819894	RTA22200255F.d.09.1.P.Seq	F	M00063931B:E10	CH21PRN
267	827355	RTA22200266F.e.07.1.P.Seq	F	M00064601C:G07	CH22PRC
268	372718	RTA22200256F.l.03.1.P.Seq	F	M00064122C:B06	CH21PRN
269	647435	RTA22200251F.b.10.1.P.Seq	F	M00063156D:H10	CH21PRN
270	450262	RTA22200265F.a.10.1.P.Seq	F	M00064514A:G10	CH22PRC
271	484703	RTA22200255F.i.20.1.P.Seq	F	M00064032D:G04	CH21PRN
272	819498	RTA22200256F.f.12.1.P.Seq	F	M00064089B:F09	CH21PRN
273	406043	RTA22200263F.i.12.1.P.Seq	F	M00064404A:B05	CH22PRC
274	817500	RTA22200255F.f.24.1.P.Seq	F	M00063945A:C03	CH21PRN
275	818180	RTA22200264F.o.18.1.P.Seq	F	M00064506A:C07	CH22PRC
276	818143	RTA22200251F.a.03.1.P.Seq	F	M00063151A:G06	CH21PRN
277	819756	RTA22200267F.a.18.1.P.Seq	F	M00064649A:E04	CH22PRC
278	406908	RTA22200257F.i.18.3.P.Seq	F	M00064176D:H10	CH21PRN
279	124863	RTA22200256F.o.21.2.P.Seq	F	M00064136C:D12	CH21PRN
280	429009	RTA22200257F.e.24.1.P.Seq	F	M00064161B:G04	CH21PRN
281	402586	RTA22200257F.i.24.3.P.Seq	F	M00064178B:A05	CH21PRN
282	400475	RTA22200254F.i.04.1.P.Seq	F	M00063890A:H04	CH21PRN
283	403453	RTA22200264F.d.12.1.P.Seq	F	M00064450C:E07	CH22PRC
284	383021	RTA22200259F.d.06.1.P.Seq	F	M00063534C:A02	CH22PRC
285	394913	RTA22200254F.p.10.1.P.Seq	F	M00063915C:E01	CH21PRN
286	831361	RTA22200263F.k.19.1.P.Seq	F	M00064414D:D06	CH22PRC
287	646020	RTA22200267F.n.21.1.P.Seq	F	M00064723C:H04	CH22PRC

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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290	402586	RTA22200257F.j.01.3.P.Seq	F	M00064178B:A05	CH21PRN
291	400475	RTA22200262F.j.21.1.P.Seq	F	M00064349D:H01	CH22PRC
292	818937	RTA22200262F.h.14.2.P.Seq	F	M00064341A:C02	CH22PRC
293	557697	RTA22200261F.j.20.1.P.Seq	F	M00064018C:E07	CH22PRC
294	831361	RTA22200265F.m.24.1.P.Seq	F	M00064569B:A09	CH22PRC
295	194490	RTA22200252F.c.10.1.P.Seq	F	M00063520D:D08	CH21PRN
296	818143	RTA22200254F.b.18.1.P.Seq	F	M00063848C:G11	CH21PRN
297	377286	RTA22200259F.a.10.1.P.Seq	F	M00063163A:G04	CH22PRC
298	831361	RTA22200265F.n.01.1.P.Seq	F	M00064569B:A09	CH22PRC
299	385307	RTA22200255F.p.07.1.P.Seq	F	M00064060B:D03	CH21PRN
300	378447	RTA22200251F.c.01.1.P.Seq	F	M00063158A:E11	CH21PRN
301	378447	RTA22200251F.b.24.1.P.Seq	F	M00063158A:E11	CH21PRN
302	817514	RTA22200260F.m.17.1.P.Seq	F	M00063968D:G08	CH22PRC
303	818942	RTA22200255F.f.03.1.P.Seq	F	M00063941B:C12	CH21PRN
304	818942	RTA22200267F.e.23.1.P.Seq	F	M00064678D:F05	CH22PRC
305	817363	RTA22200266F.f.04.1.P.Seq	F	M00064605C:G05	CH22PRC
306	818942	RTA22200255F.i.02.1.P.Seq	F	M00064025D:E07	CH21PRN
307	818942	RTA22200265F.g.23.1.P.Seq	F	M00064534D:F06	CH22PRC
308	817457	RTA22200267F.e.15.1.P.Seq	F	M00064675C:E09	CH22PRC
309	831968	RTA22200263F.f.23.1.P.Seq	F	M00064393B:H04	CH22PRC
310	530941	RTA22200253F.h.05.1.P.Seq	F	M00063785C:F03	CH21PRN
311	763446	RTA22200257F.j.05.3.P.Seq	F	M00064179A:C04	CH21PRN
312	763446	RTA22200255F.n.21.1.P.Seq	F	M00064053D:F02	CH21PRN
313	819219	RTA22200256F.f.16.1.P.Seq	F	M00064090C:A02	CH21PRN
314	763446	RTA22200258F.b.19.2.P.Seq	F	M00064248A:E02	CH21PRN
315	10154				
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Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
19	<NONE>	<NONE>	<NONE>	1077580	hypothetical protein YDR125c - yeast	7
20	<NONE>	<NONE>	<NONE>	4585925	(AC007211) unknown protein	6
21	<NONE>	<NONE>	<NONE>	1085306	EVI1 protein - human	4.3
22	<NONE>	<NONE>	<NONE>	3876587	(Z81521) predicted using Genefinder; cDNA EST yk233g4.5 comes from this gene; cDNA EST yk233g4.3 comes from this gene [Caenorhabditis elegans]	0.85
23	<NONE>	<NONE>	<NONE>	1086591	(U41007) similar to S. cervisiae nuclear protein SNF2	0.34
24	<NONE>	<NONE>	<NONE>	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	0.29
25	<NONE>	<NONE>	<NONE>	2633160	(Z99108) similar to surface adhesion YfiQ [Bacillus subtilis]	0.19
26	<NONE>	<NONE>	<NONE>	755468	(U19879) transmembrane protein [Xenopus laevis]	0.042
27	<NONE>	<NONE>	<NONE>	4507339	T brachyury (mouse) homolog protein [Homo sapiens]	0.029

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
28	<NONE>	<NONE>	<NONE>	729711	PROTEASE DEGS PRECURSOR 3.4.21.-) hhoB - Escherichia coli >gi|558913 (U15661) HhoB [Escherichia coli] >gi|606174 (U18997) ORF_o355 coli] >gi|1789630 (AE000402) protease [Escherichia coli]	0.004
29	<NONE>	<NONE>	<NONE>	3168911	(AF068718) No definition line found [Caenorhabditis elegans]	8e-013
30	<NONE>	<NONE>	<NONE>	2832777	(AL021086) /prediction=(method:; comes from the 5' UTR [Drosophila melanogaster]	3e-040
31	X78712	H.sapiens mRNA for glycerol kinase testis specific 2	2.1	2852449	(D88207) protein kinase [Arabidopsis thaliana] >gi|2947061 (AC002521) putative protein kinase	9.1
32	X60760	L.esculentum TDR8 mRNA	2.1	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
33	U40853	Oryctolagus cuniculus pulmonary surfactant protein B (SP-B) gene, complete cds	2	<NONE>	<NONE>	<NONE >
34	AF083655	Homo sapiens procollagen C-proteinase enhancer protein (PCOLCE) gene, 5' flanking region and complete cds	2	<NONE>	<NONE>	<NONE >
35	AJ223776	Staphylococcus warneri hld gene	2	<NONE>	<NONE>	<NONE >
36	U40853	Oryctolagus cuniculus pulmonary surfactant protein B (SP-B) gene, complete cds	2	<NONE>	<NONE>	<NONE >
37	X04436	Clostridium tetani gene for tetanus toxin	2	<NONE>	<NONE>	<NONE >
38	Z35787	S.cerevisiae chromosome II reading frame ORF YBL026w	2	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	8.4
39	X78712	H.sapiens mRNA for glycerol kinase testis specific 2	2	2852449	(D88207) protein kinase [Arabidopsis thaliana] >gi|2947061 (AC002521) putative protein kinase	8.2

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
40	Z15056	B.subtilis genes spoVD, murE, mraY, murD	2	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	2.8
41	S65623	cAMP-regulated enhancer-binding protein 1 of 3]	2	119266	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) regulatory protein elf-1 - fruit fly (Drosophila melanogaster) >gi|7939|emb |CAA33692| (X15657) Elf-1 protein (AA 1-1063) [Drosophila melanogaster]	0.55
42	NM_004415 .1	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA mRNA, complete cds	2	2649177	(AE001008) conserved hypothetical protein [Archaeoglobus fulgidus]	0.2
43	AF031552	Vibrio cholerae magnesium transporter (mgtE) gene, partial cds; sensor kinase (vieS), response regulator (vieA), and response regulator (vieB) genes, complete cds; and collagenase (vcc) gene,	2	2088714	(AF003139) strong similarity to NADPH oxidases; partial CDS, the gene begins in the neighboring clone	2e-013

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
		(vcc) gene, partial cds				
44	AF116852.1	Danio rerio dickkopf-1 (dkk1) mRNA, complete cds	2	3800951	(AF100657) No definition line found [Caenorhabditis elegans]	2e-019
45	X82595	P.sativum fuc gene	1.9	<NONE>	<NONE>	<NONE>
46	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1.9	<NONE>	<NONE>	<NONE>
47	AF130672.1	Felis catus clone Fca603 microsatellite sequence	1.9	<NONE>	<NONE>	<NONE>
48	AJ007044	Oryctolagus Cuniculus sod gene	1.9	388055	(L22981) merozoite surface protein-1 [Plasmodium chabaudi]	7.8
49	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	1.9	160925	(M94346) A.1.12/9 antigen [Schistosoma mansoni]	7.7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
50	U30290	Rattus norvegicus galanin receptor GALR1 mRNA, complete cds	1.9	3024079	GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN) (L36LBP) >gi|2281707 sapiens] >gi|2623387 (U82953) galectin-4 [Homo sapiens]	4.5
51	Y13234	Chironomus tentans mRNA for chitinase, 1695 bp	1.9	4567068	(AF125568) tumor suppressing STF cDNA 4 [Homo sapiens]	3.4
52	NM_003644 .1	Homo sapiens growth arrest-specific 7 (GAS7) mRNA > :: emb|AJ224876| HSAJ4876 Homo sapience mRNA for GAS7 protein	1.9	125560	PROTEIN KINASE C, GAMMA TYPE C (EC 2.7.1.-) gamma - rabbit >gi|165652 (M19338) protein kinase delta [Oryctolagus cuniculus]	0.53
53	AB013448.1	Oryza sativa gene for Pib, complete cds	1.8	<NONE>	<NONE>	<NONE >
54	D63854	Human cytomegalovirus DNA,replication origin	1.8	<NONE>	<NONE>	<NONE >
55	AB002340	Human mRNA for KIAA0342 gene, complete cds	1.8	<NONE>	<NONE>	<NONE >
56	AF017779	Mus musculus vitamin D receptor gene, promoter region	1.8	<NONE>	<NONE>	<NONE >

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
57	D63854	Human cytomegalovirus DNA,replication origin	1.8	<NONE>	<NONE>	<NONE >
58	M24102	Bovine ADP/ATP translocase T1 mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE >
59	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	1.8	<NONE>	<NONE>	<NONE >
60	M37394	Rat epidermal growth factor receptor mRNA.	1.8	<NONE>	<NONE>	<NONE >
61	AF006304	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds	1.8	<NONE>	<NONE>	<NONE >
62	D13454	Candida albicans CACHS3 gene for chitin synthase III	1.8	<NONE>	<NONE>	<NONE >
63	Y00354	Xenopus laevis gene encoding vitellogenin A2	1.8	1077580	hypothetical protein YDR125c - yeast	7.5
64	U90936	Aspergillus niger px27 gene, promoter region	1.8	4337033	(AF124138) transcriptional activator protein CdaR [Streptomyces coelicolor] transcriptional regulator [Streptomyces coelicolor]	7.3

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
65	D84448	Cavia cobaya mRNA for Na+,K+-ATPase beta-3 subunit, complete cds	1.8	4704603	(AF109916) putative dehydrin	7.1
66	AF039948	Xenopus laevis clone H-0 transcription elongation factor S-II (TFIIS) precursor RNA, isoform TFIIS.h, partial cds	1.8	1695839	(U58151) envelope glycoprotein [Human immunodeficiency virus type 1]	5.6
67	M18061	Xenopus laevis vitelloginin gene, complete cds.	1.8	780502	(U18466) AP endonuclease class II [African swine fever virus] >gi|1097525|prf||2113434ET AP endonuclease:ISOTYPE=class II [African swine fever virus]	3.1
68	U61112	Mus musculus Eya3 homolog mRNA, complete cds	1.8	3043646	(AB011133) KIAA0561 protein [Homo sapiens]	1.9
69	AB018442	Oryza sativa mRNA for phytochrome C, complete cds	1.8	4455041	(AF116463) unknown [Streptomyces lincolnensis]	0.49

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
70	D63854	Human cytomegalovirus DNA,replication origin	1.8	1169200	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR >gi|421829|pir||S33706 DNA-damage resistance protein - Arabidopsis thaliana and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]	0.22
71	D26549	Bovine mRNA for adseverin, complete cds	1.8	755468	(U19879) transmembrane protein [Xenopus laevis]	0.042
72	J05211	Human desmoplakin mRNA, 3' end.	1.8	728867	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi|99694|pir||S21961 proline-rich protein APG - Arabidopsis thaliana >gi|22599|emb|CAA42925|	0.015

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
73	NM_004415 .1	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA mRNA, complete cds	1.8	728867	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi|99694|pir||S21961 proline-rich protein APG - Arabidopsis thaliana >gi|22599|emb|CAA42925|	0.015
74	AF038604	Caenorhabditis elegans cosmid B0546	1.8	3877951	(Z81555) predicted using Genefinder	3e-008
75	AF038604	Caenorhabditis elegans cosmid B0546	1.8	3877951	(Z81555) predicted using Genefinder	2e-011
76	U23551	Prochlorothrix hollandica phosphomannomutase	1.8	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|emb|CAA16762| (AL021711) putative protein [Arabidopsis thaliana]	2e-013
77	S60150	ORF1...ORF6 {3' terminal reigon} [chrysanthemum virus B CVB, Genomic RNA, 6 genes, 3426 nt]	1.8	1065454	(U40410) C54G7.2 gene product [Caenorhabditis elegans]	2e-019
78	AB014558	Homo sapiens mRNA for KIAA0658 protein, partial cds	1.8	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	6e-027

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
79	X17191	E.gracilis chloroplast RNA polymerase rpoB-rpoC1-rpoC2 operon	1.7	<NONE>	<NONE>	<NONE>
80	X07729	R.norvegicus gene encoding neuron-specific enolase, exons 8-12	1.7	4584544	(AL049608) extensin-like protein	8.8
81	D38178	Human gene for cytosolic phospholipase A2, exon 1	1.7	73714	infected cell protein ICP34.5 - human herpesvirus 1 (strain F) >gi|330123 (M12240) infected cell protein [Herpes simplex virus type 1]	1.1
82	U23551	Prochlorothrix hollandica phosphomannomutase	1.7	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi|2832633|emb|CAA16762| (AL021711) putative protein [Arabidopsis thaliana]	2e-010
83	Y00525	Klebsiella pneumoniae nifL gene for regulatory protein	1.6	3800951	(AF100657) No definition line found [Caenorhabditis elegans]	6e-013
84	AF100170.1	Bos taurus major fibrous sheath protein precursor, mRNA, complete cds	1.5	463552	(U05877) AF-1 [Homo sapiens]	0.074
85	Y13441	Homo sapiens Rox gene, exon 2	0.74	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)		.	Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
86	L46792	Actinidia deliciosa clone AdXET-5 xyloglucan endotransglycosylase precursor (XET) mRNA, complete cds	0.73	3170252	(AF043636) circumsporozoite protein [Plasmodium chabaudi]	0.001
87	U73489	Drosophila melanogaster Nem (nem) mRNA, complete cds	0.7	3915994	HYPOTHETICAL 53.2 KD PROTEIN IN PRC-PRPA INTERGENIC REGION	3e-005
88	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.68	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	8.5
89	AF082012	Caenorhabditis elegans UDP-N-acetylglucosamine:a-3-D-mannoside b-1,2-N-acetylglucosaminyltransferase I (gly-14) mRNA, complete cds	0.67	2494313	PUTATIVE TRANSLATION INITIATION FACTOR EIF-2B SUBUNIT 1 (EIF-2B GDP-GTP EXCHANGE FACTOR) eIF-2B, subunit alpha - Methanococcus jannaschii aIF-2B, subunit delta (aIF2BD) [Methanococcus jannaschii]	8.4
90	U04354	Mus musculus ADSEVERIN mRNA, complete cds	0.67	4755188	(AC007018) unknown protein	8e-026

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
91	M68881	S.pombe cigl+ gene, complete cds.	0.67	2078441	(U56964) weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386)	2e-030
92	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.66	2829685	PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (R-PTP-X) (PTP IA-2BETA) (PROTEIN TYROSINE PHOSPHATASE-NP) (PTP-NP) >gi|1515425 (U57345) protein tyrosine phosphatase-NP [Mus musculus]	6.2
93	Z15056	B.subtilis genes spoVD, murE, mraY, murD	0.66	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	2.1
94	M86808	Human pyruvate dehydrogenase complex (PDHA2) gene, complete cds.	0.65	<NONE>	<NONE>	<NONE>
95	J03754	Rat plasma membrane Ca2+ ATPase-isoform 2 mRNA, complete cds.	0.65	4507549	transmembrane protein with EGF-like and two follistatin-like domains 1 >gi|755466	8e-006

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
96	NM_000887.1	Homo sapiens integrin, alpha X (antigen CD11C emb|Y00093|HSP15095 H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.64	<NONE>	<NONE>	<NONE>
97	L27080	Human melanocortin 5 receptor (MC5R) gene, complete cds.	0.64	<NONE>	<NONE>	<NONE>
98	U07890	Mus musculus C57BL/6J epidermal surface antigen (mesa) mRNA, complete cds.	0.64	<NONE>	<NONE>	<NONE>
99	AF079139	Streptomyces venezuelae pikCD operon, complete sequence	0.64	3041869	(U96109) proline-rich transcription factor ALX3 [Mus musculus]	2.8
100	M16140	Chicken ovoinhibitor gene, exon 15.	0.64	123984	ACROSIN INHIBITORS IIA AND IIB	4e-008
101	NM_000887.1	Homo sapiens integrin, alpha X (antigen CD11C emb|Y00093|HSP15095 H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.63	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
102	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.63	<NONE>	<NONE>	<NONE>
103	Z25470	H.sapiens melanocortin 5 receptor gene, complete CDS	0.63	<NONE>	<NONE>	<NONE>
104	L19954	Bacillus subtilis feuA, B, and C genes, 3 ORFs, 2 complete cds's and 5'end.	0.63	<NONE>	<NONE>	<NONE>
105	U44405	Spiroplasma citri chromosome pre-inversion border, SPV1-like sequences, transposase gene, partial cds, adhesin-like protein P58 gene, complete cds.	0.63	2499642	SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG >gi|1737181 (U73457) Cst20p [Candida albicans]	7.7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
106	Z28264	S.cerevisiae chromosome XI reading frame ORF YKR039w	0.63	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T00805 ...	2e-014
107	AE001107	Archaeoglobus fulgidus section 172 of 172 of the complete genome	0.62	<NONE>	<NONE>	<NONE>
108	Z14112	B.firmus TopA gene encoding DNA topoisomerase I	0.62	310115	(L02530) Drosophila polarity gene (frizzled) homologue	0.026
109	AF118101	Toxoplasma gondii protein kinase 6 (tpk6) mRNA, complete cds	0.62	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	4e-018
110	M59743	Rabbit cardiac muscle Ca-2+ release channel	0.61	<NONE>	<NONE>	<NONE>
111	M12036	Human tyrosine kinase-type receptor (HER2) gene, partial cds.	0.61	61962	(X58484) gag [Simian foamy virus]	7.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs.. Non-Redundant Proteins)		
112	AF043195	Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A	0.61	1572629	(U69699) unknown protein precursor [Mus musculus]	7.5
113	U18178	Human HLA class I genomic survey sequence.	0.61	1336688	(S81116) properdin [guinea pigs, spleen, Peptide, 470 aa] [Cavia]	5.7
114	U44405	Spiroplasma citri chromosome pre-inversion border, SPV1-like sequences, transposase gene, partial cds, adhesin-like protein P58 gene, complete cds.	0.61	2827531	(AL021633) hypothetical protein	3.3
115	Z33011	M.capricolum DNA for CONTIG MC008	0.61	3915729	HYPERPLASTIC DISCS PROTEIN (HYD PROTEIN) >gi|2673887 (L14644) hyperplastic discs protein	0.26
116	NM_001429.1	Homo sapiens E1A binding protein p300 mRNA, complete cds. > :: gb|I62297|I62297 Sequence 1 from patent US 5658784	0.61	4204294	(AC003027) lcl|prt_seq No definition line found	5e-005

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
117	Z25418	C.familiaris MHC class Ib gene (DLA-79) gene, complete CDS	0.61	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	1e-007
118	AB002150	Bacillus subtilis DNA for FeuB, FeuA, YbbB, YbbC, YbbD, YbzA, YbbE, YbbF, YbbH, YbbI, YbbJ, YbbK, YbbL, YbbM, YbbP, complete cds	0.6	<NONE>	<NONE>	<NONE>
119	Y07786	V.cholerae ORF's involved in lipopolysaccharide synthese	0.6	<NONE>	<NONE>	<NONE>
120	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.6	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
121	Z71403	S.cerevisiae chromosome XIV reading frame ORF YNL127w	0.6	<NONE>	<NONE>	<NONE>
122	L34641	Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exon 10.	0.6	1147634	(U42213) micronemal TRAP-C1 protein homolog	9.6
123	AF070572	Homo sapiens clone 24778 unknown mRNA	0.6	399034	N-ACETYLMURAMOYL-L-ALANINE AMIDASE AMIB PRECURSOR >gi|628763|pir||S41741 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - Escherichia coli >gi|304914 (L19346) N-acetylmuramoyl-L-alanine amidase [Escherichia coli] N-acetylmuramoyl-l-alanine amidase II; a	2.5
124	X75627	C.burnetii trxB, spoIIIE and serS genes	0.6	3036833	(AJ003163) apsB [Emericella nidulans]	0.28
125	Z99765	Flaveria pringlei gdcsH gene	0.59	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
126	U02538	Mycoplasma hyopneumoniae J ATCC 25934 23S rRNA gene, partial sequence	0.59	<NONE>	<NONE>	<NONE>
127	Z71403	S.cerevisiae chromosome XIV reading frame ORF YNL127w	0.59	<NONE>	<NONE>	<NONE>
128	X03942	Mouse simple repetitive DNA (sqr family) transcript (clone pmlc 2) with conserved GACA/GATA repeats	0.59	<NONE>	<NONE>	<NONE>
129	U11844	Mus musculus glucose transporter (GLUT3) gene, exon 1	0.59	<NONE>	<NONE>	<NONE>
130	D63395	Homo sapiens mRNA for NOTCH4, partial cds	0.59	4433616	(AF107018) alpha-mannosidase IIx [Mus musculus]	1.8
131	Z33011	M.capricolum DNA for CONTIG MC008	0.59	3915729	HYPERPLASTIC DISCS PROTEIN (HYD PROTEIN) >gi|2673887 (L14644) hyperplastic discs protein	0.27
132	U05670	Haemophilus influenzae DL42 Lex2A and Lex2B genes, complete cds.	0.58	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
133	L27080	Human melanocortin 5 receptor (MC5R) gene, complete cds.	0.58	123984	ACROSIN INHIBITORS IIA AND IIB	2e-006
134	AF043195	Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A	0.57	1572629	(U69699) unknown protein precursor [Mus musculus]	6.7
135	U57707	Bos taurus activin receptor type IIB precursor	0.57	807646	(M17294) unknown protein [Human herpesvirus 4]	0.068
136	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.56	<NONE>	<NONE>	<NONE>
137	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	0.56	<NONE>	<NONE>	<NONE>
138	M64932	Candida maltosa cyclohexamide resistance protein	0.56	3219524	(AF069428) NADH dehydrogenase subunit IV [Alligator mississippiensis] >gi|3367630|emb|CAA73570| (Y13113) NADH dehydrogenase subunit 4 [Alligator mississippiensis]	1.3

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
139	AE000342	Escherichia coli K-12 MG1655 section 232 of 400 of the complete genome	0.56	3874685	(Z78539) Similarity to S.pombe hypothetical protein C4G8.04 (SW:YAD4_SCHPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come...	0.088
140	Z15056	B.subtilis genes spoVD, murE, mraY, murD	0.55	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	3.7
141	Z58167	H.sapiens CpG island DNA genomic Mse1 fragment, clone 30e10, forward read cpg30e10.ft1b	0.53	<NONE>	<NONE>	<NONE>
142	M27159	Rat potassium channel-Kv2 gene, partial cds.	0.53	1850920	(U21247) Bet [Human spumaretrovirus]	0.9
143	M15555	Mouse Ig germline V-kappa-24 chain (VK24C) gene, exons 1 and 2.	0.24	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
144	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.24	399109	TRANSCRIPTION FACTOR BF-1 (BRAIN FACTOR 1) (BF1) >gi|92020|pir||JH0672 brain factor 1 protein - rat >gi|203135 (M87634) BF-1 [Rattus norvegicus]	4
145	AJ002014	Crythecodinium cohnii mRNA for nuclear protein JUS1	0.24	416704	BALBIANI RING PROTEIN 3 PRECURSOR balbiani ring 3 (BR3) [Chironomus tentans]	0.36
146	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.23	1388158	(U58204) myomesin [Gallus gallus]	8.8
147	NM_001432.1	Homo sapiens epiregulin (EREG) mRNA > :: dbj|D30783|D30783 Homo sapiens mRNA for epiregulin, complete cds	0.23	2851520	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF) (ETGF) (TGF TYPE 1) precursor - rat >gi|207282 (M31076) transforming growth factor alpha precursor [Rattus norvegicus]	2e-008

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
148	U57043	Cebus apella gamma globin (gamma1) gene, complete cds	0.22	<NONE>	<NONE>	<NONE >
149	AB023188.1	Homo sapiens mRNA for KIAA0971 protein, complete cds	0.22	<NONE>	<NONE>	<NONE >
150	M18105	Yeast (S.cerevisiae) SST2 gene encoding desensitization to alpha- factor pheromone, complete cds.	0.22	<NONE>	<NONE>	<NONE >
151	AJ001113	Homo sapiens UBE3A gene, exon 16	0.22	3122961	ENHANCER OF SPLIT GROUCHO-LIKE PROTEIN 1 >gi|2408145 (U18775) enhancer of split groucho	8.5
152	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.22	1388158	(U58204) myomesin [Gallus gallus]	8.1
153	D42042	Human mRNA for KIAA0085 gene, partial cds	0.22	4827063	zinc finger protein 142 (clone pHZ-49) >gi|3123312|sp|P52746|Z142_HUMAN ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654) >gi|1510147|dbj|BAA13242|	6.1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
154	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.22	2853301	(AF007194) mucin [Homo sapiens]	1.6
155	Z11653	H.sapiens DBH gene complex repeat polymorphism DNA	0.22	3819705	(AL032824) syntaxin binding protein 1; sec1 family secretory protein [Schizosaccharomyces pombe]	1.2
156	L29063	Candida albicans fatty acid synthase alpha subunit (FAS2) gene, complete cds.	0.22	3046871	(AB003753) high sulfur protein B2E [Rattus norvegicus]	0.32
157	M64865	Horse alcohol dehydrogenase-S-isoenzyme mRNA, complete cds.	0.22	2213909	(AF004874) latent TGF-beta binding protein-2 [Mus musculus]	0.037
158	Y09472	B.taurus gene encoding preprododecapeptide	0.21	2909874	(AF047829) melatonin-related receptor [Ovis aries]	7.6
159	Y09472	B.taurus gene encoding preprododecapeptide	0.21	2909874	(AF047829) melatonin-related receptor [Ovis aries]	7.5
160	X80301	N.tabacum axi 1 gene	0.21	2832715	(AJ003066) subunit beta of the mitochondrial fatty acid beta-oxydation multienzyme complex [Bos taurus]	6

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
161	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	0.21	2224559	(AB002307) KIAA0309 [Homo sapiens]	3.3
162	S78251	growth hormone receptor {alternatively spliced, exon 1B} [sheep, Merino, skeletal muscle, mRNA. Partial, 438 nt]	0.21	729381	DYNAMIN-1 (DYNAMIN BREDNM19)	2
163	U16135	Synechococcus sp. Clp protease proteolytic subunit	0.21	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.02
164	X95601	M.hominis lmp3 and lmp4 genes	0.21	2995445	(Y10496) CDV-1 protein [Mus musculus]	0.005
165	X95601	M.hominis lmp3 and lmp4 genes	0.21	2995447	(Y10495) CDV-1R protein [Mus musculus]	0.005
166	AF124249.1	Homo sapiens SH2-containing protein Nsp1 mRNA, complete cds	0.21	423456	epidermal growth factor-receptor-binding protein GRB-4 - mouse (fragment)	8e-010
167	AF030282	Danio rerio homeobox protein Six7 (six7) mRNA, complete cds	0.21	3928083	(AC005770) unknown protein [Arabidopsis thaliana]	2e-014
168	X83427	O.anatinus mitochondrial DNA, complete genome	0.21	132575	RIBONUCLEASE INHIBITOR	3e-021

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
169	AJ001113	Homo sapiens UBE3A gene, exon 16	0.2	<NONE>	<NONE>	<NONE>
170	AF081533.1	Anopheles gambiae putative gram negative bacteria binding protein gene, complete cds	0.2	<NONE>	<NONE>	<NONE>
171	U70316	Dictyostelium discoideum IonA (iona) gene, partial cds	0.2	<NONE>	<NONE>	<NONE>
172	AF009341	Homo sapiens E6-AP ubiquitin-protein ligase	0.2	<NONE>	<NONE>	<NONE>
173	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.2	3702275	(AC005793) KIAA0561 protein [AA 1-593] [Homo sapiens]	2.5
174	AE000573.1	Helicobacter pylori 26695 section 51 of 134 of the complete genome	0.2	3947855	(AL034381) putative Golgi membrane protein	2.5
175	X83230	G.gallus hsp90beta gene	0.2	3258596	(U95821) putative transmembrane GTPase [Drosophila melanogaster]	0.81
176	X57157	Chicken mRNA for Hsp47, heat shock protein 47	0.2	108325	insulin-like growth factor-binding protein 6	0.17

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
177	M58748	Chicken alpha-globin gene domain with structural matrix attachment sites.	0.2	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-005
178	AB016815	Anthocidaris crassispina mRNA for Src-type protein tyrosine kinase, complete cds	0.2	423456	epidermal growth factor-receptor-binding protein GRB-4 - mouse (fragment)	1e-012
179	AF030282	Danio rerio homeobox protein Six7 (six7) mRNA, complete cds	0.2	3928083	(AC005770) unknown protein [Arabidopsis thaliana]	3e-014
180	AL035559	Streptomyces coelicolor cosmid 9F2	0.2	2088714	(AF003139) strong similarity to NADPH oxidases; partial CDS, the gene begins in the neighboring clone	3e-022
181	S79641	SDH=succinate dehydrogenase flavoprotein subunit Mutant, 387 nt]	0.2	4755188	(AC007018) unknown protein	2e-022
182	X75383	H.sapiens mRNA for TFIIA-alpha	0.19	<NONE>	<NONE>	<NONE>
183	U53901	Hippopotamus amphibius b-casein gene, exon 7, partial cds	0.19	<NONE>	<NONE>	<NONE>
184	J05265	Mouse interferon gamma receptor mRNA, complete cds.	0.19	77356	hypothetical 70K protein - eggplant mosaic virus	0.0005

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
185	U72353	Rattus norvegicus lamin B1 mRNA, complete cds	0.19	3880857	(AL031633) cDNA EST yk404d1.5 comes from this gene; cDNA EST yk404d1.3 comes from this gene	2e-006
186	AB016815	Anthocidaris crassispina mRNA for Src-type protein tyrosine kinase, complete cds	0.19	3930217	(AF047487) Nck-2 [Homo sapiens]	2e-007
187	D10911	Mus musculus DNA for MS2 protein, complete cds	0.19	2662366	(D86332) membrane type-2 matrix metalloproteinase [Mus musculus]	5e-011
188	AB015345	Homo sapiens HRIHFB2216 mRNA, partial cds	0.075	3877417	(Z66564) similar to anion exchange protein	6.4
189	AF086410	Homo sapiens full length insert cDNA clone ZD77B03	0.075	3023371	PHEROMONE B BETA 1 RECEPTOR	4.9
190	K02024	Human T-cell lymphotropic virue type II env gene encoding envelope glycoprotein, complete cds.	0.075	2791527	(AL021246) PE_PGRS [Mycobacterium tuberculosis]	0.11

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
191	M10188	X.laevis mitochondrial DNA containing the D-loop, and the 12S rRNA, apocytochrome b, Glu-tRNA, Thr-tRNA, Pro-tRNA and Phe-tRNA genes.	0.074	4753163	huntingtin DISEASE PROTEIN) (HD PROTEIN) >gi|454415 (L12392) Huntington's Disease protein [Homo sapiens]	2.8
192	X85525	G.gallus AG repeat region (GgaMU130)	0.073	984339	(U20966) Rev [Simian immunodeficien cy virus]	3.6
193	AJ238394.1	Homo sapiens AML2 gene (partial)	0.07	4240219	(AB020672) KIAA0865 protein [Homo sapiens]	2
194	AF039704	Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds	0.069	2894106	(Z78279) Collagen alpha1 [Rattus norvegicus]	0.39
195	K02024	Human T-cell lymphotropic virue type II env gene encoding envelope glycoprotein, complete cds.	0.068	4504857	potassium intermediate/sm all conductance calcium-activated channel, subfamily N, member 3 >gi|3309531 (AF031815) calcium-activated potassium channel [Homo sapiens]	0.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
196	Z60719	H.sapiens CpG island DNA genomic Mse1 fragment, clone 33a11, forward read cpg33a11.ft1m	0.068	4826874	nucleoporin 214kD (CAIN) PROTEIN NUP214 (NUCLEOPORIN NUP214) (214 KD NUCLEOPORIN) transforming protein (can) - human sapiens]	0.044
197	AF053994	Lycopersicon esculentum Hcr2-0A (Hcr2-0A) gene, complete cds	0.068	2842699	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE)	9e-009
198	AJ233650.1	Equus caballus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Horse1	0.067	<NONE>	<NONE>	<NONE>
199	M10188	X.laevis mitochondrial DNA containing the D-loop, and the 12S rRNA, apocytochrome b, Glu-tRNA, Thr-tRNA, Pro-tRNA and Phe-tRNA genes.	0.067	4753163	huntingtin DISEASE PROTEIN) (HD PROTEIN) >gi|454415 (L12392) Huntington's Disease protein [Homo sapiens]	2.5

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
200	U14646	Murine hepatitis virus Y strain S glycoprotein gene, complete cds.	0.067	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T00805 ...	1e-019
201	X15373	Mouse cerebellum mRNA for P400 protein	0.066	164507	(M81771) immunoglobulin gamma-chain [Sus scrofa]	9.4
202	AF086410	Homo sapiens full length insert cDNA clone ZD77B03	0.066	3023371	PHEROMONE B BETA 1 RECEPTOR	4.2
203	AL034492	Streptomyces coelicolor cosmid 6C5	0.066	3800951	(AF100657) No definition line found [Caenorhabditis elegans]	3e-015
204	L13377	Staphylococcus aureus enterotoxin gene, 3' end.	0.065	<NONE>	<NONE>	<NONE>
205	U83478	Thelephoraceae sp. 'Taylor #13' ITS1, 5.8S ribosomal RNA gene, and ITS2, complete sequence	0.065	3877335	(Z92786) predicted using Genefinder	9.1

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
206	AJ002014	Crythecodinium cohnii mRNA for nuclear protein JUS1	0.065	1213283	(U40576) SIM2 [Mus musculus]	0.47
207	AB016804	Aloe arborescens mRNA for NADP-malic enzyme, complete cds	0.065	2832777	(AL021086) /prediction=(method:; comes from the 5' UTR [Drosophila melanogaster]	5e-036
208	AJ002014	Crythecodinium cohnii mRNA for nuclear protein JUS1	0.063	1213283	(U40576) SIM2 [Mus musculus]	0.45
209	AB023143.1	Homo sapiens mRNA for KIAA0926 protein, complete cds	0.024	132575	RIBONUCLEASE INHIBITOR	8e-026
210	U72966	Human hepatocyte nuclear factor 4-alpha gene, exon 7	0.022	<NONE>	<NONE>	<NONE>
211	X02801	Mouse gene for glial fibrillary acidic protein	0.022	2231607	(U85917) nef protein [Human immunodeficiency virus type 1]	7
212	AF017636	Mesocricetus auratus 3-keto-steroid reductase	0.022	2723362	(AF023459) lustrin A [Haliotis rufescens]	0.097
213	Z36879	F.pringlei gdcsPA gene for P-protein of the glycine cleavage system	0.008	<NONE>	<NONE>	<NONE>
214	X73150	P.sativum GapC1 gene	0.008	1572629	(U69699) unknown protein precursor [Mus musculus]	8.6

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
215	AJ239031.1	Homo sapiens LSS gene, partial, exons 22, 23 and joined CDS	0.008	4508019	zinc finger protein 231 protein [Homo sapiens]	0.01
216	U76602	Human 180 kDa bullous pemphigoid antigen 2/type XVII collagen (BPAG2/COL17A1) gene, exons 49, 50, 51 and 52	0.007	3170252	(AF043636) circumsporozoite protein [Plasmodium chabaudi]	0.0001
217	M11283	Aplysia californica FMRFamide mRNA, partial cds, clone FMRF-2.	0.007	3874685	(Z78539) Similarity to S.pombe hypothetical protein C4G8.04 (SW:YAD4_SCHPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come...	9e-013
218	J03998	P.falciparum glutamic acid-rich protein gnen, complete cds.	0.003	<NONE>	<NONE>	<NONE>
219	Z23143	M.musculus ALK-6 mRNA, complete CDS	0.002	2393890	(AF006064) protein kinase homolog [Fowlpox virus]	1e-011

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
220	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	0.001	2136964	cysteine-rich hair keratin associated protein - rabbit >gi|510541|emb|CAA56339 | (X80035) cysteine rich hair keratin associated protein	1.9
221	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.0008	3687246	(AC005169) putative suppressor protein [Arabidopsis thaliana]	5.5
222	L41608	Methylobacterium extorquens (clone pDN9, HINDIIIAB) mxaS gene 3' end, mxaA, mxaC, mxaK, mxaL and mxaD genes, complete cds.	0.0008	3024235	NERVOUS-SYSTEM SPECIFIC OCTAMER-BINDING TRANSCRIPTION FACTOR N-OCT 3 PROTEIN)	5.1
223	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	0.0008	2136964	cysteine-rich hair keratin associated protein - rabbit >gi|510541|emb|CAA56339 | (X80035) cysteine rich hair keratin associated protein	2.5
224	AC002293	Genomic sequence from Human 9q34, complete sequence [Homo sapiens]	0.0008	2789557	(AF034316) MHC class I antigen [Triakis scyllium] scyllium]	0.0002

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
225	L16013	Rattus norvegicus Q-like gene sequence	9e-005	<NONE>	<NONE>	<NONE>
226	AF148512.1	Homo sapiens hexokinase II gene, promoter region	9e-005	<NONE>	<NONE>	<NONE>
227	U94776	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	9e-005	4759138	solute carrier family 7 transporter 3 [Homo sapiens]	5.4
228	X56030	H.sapiens IAPP gene for amyloid polypeptide, exon 1	1e-005	<NONE>	<NONE>	<NONE>
229	U36515	Human CT microsatellite, clone GM5927-CT-2-3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	4e-007	2435616	(AF026215) No definition line found [Caenorhabditis elegans]	0.85
230	AB011119	Homo sapiens mRNA for KIAA0547 protein, complete cds	4e-007	4758508	airway trypsin-like protease protease [Homo sapiens]	3e-031
231	NM_000521.1	Homo sapiens hexosaminidase B (beta polypeptide) (HEXB) mRNA	5e-008	2119379	slow muscle troponin T - chicken T [Gallus gallus]	2.8
232	X13895	Human serum amyloid A (GSAA1) gene, complete cds	4e-008	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
233	AB009288.1	Homo sapiens mRNA for N-copine, complete cds	4e-008	4520342	(AB008893) N-copine [Mus musculus]	3e-006
234	AB011119	Homo sapiens mRNA for KIAA0547 protein, complete cds	4e-008	4758508	airway trypsin-like protease protease [Homo sapiens]	1e-028
235	X13895	Human serum amyloid A (GSAA1) gene, complete cds	5e-009	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.8
236	X13895	Human serum amyloid A (GSAA1) gene, complete cds	2e-009	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.2
237	U64997	Bos taurus ribonuclease K6 gene, partial cds	2e-009	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi|2745760 (AF037086) ribonuclease k6 precursor	3e-018
238	J02635	Rat liver alpha-2-macroglobulin mRNA, complete cds.	2e-009	112913	ALPHA-2-MACROGLOBULIN PRECURSOR precursor - rat >gi|202592 (J02635) prealpha-2-macroglobulin [Rattus norvegicus]	4e-019
239	Z78141	M.musculus partial cochlear mRNA (clone 29C9)	5e-010	3219569	(AL023893) /prediction=(method:;	4e-009

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
240	AF060917	Gambusia affinis microsatellite Gafu6	2e-010	3874618	(Z48241) similar to coiled coil domains; cDNA EST yk302g12.5 comes from this gene; cDNA EST yk365d10.5 comes from this gene; cDNA EST yk461c1.5 comes from this gene [Caenorhabditis elegans] coil domains; cDNA EST yk302g12.5 comes from this gene; cDNA EST	0.096
241	U68138	Human PSD-95 mRNA, partial cds	2e-010	4521241	(AB024927) CsENDO-3 [Ciona savignyi]	2e-022
242	U88827	Aotus trivirgatus ribonuclease precursor gene, complete cds	6e-011	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi|2745760 (AF037086) ribonuclease k6 precursor	1e-016
243	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	2e-012	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	3e-016

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
244	NM_001365 .1	Homo sapiens discs, large (Drosophila) homolog 4 (DLG4) mRNA > :: gb|U83192|HS U83192 Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds	2e-012	4521241	(AB024927) CsENDO-3 [Ciona savignyi]	5e-020
245	U28049	Human TBX2 (TXB2) mRNA, complete cds.	7e-013	2501115	TBX2 PROTEIN (T-BOX PROTEIN 2)	2e-011
246	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	2e-013	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-025
247	AF005963	Homo sapiens XY homologous region, partial sequence	1e-014	104270	Ig heavy chain - clawed frog	1.9
248	M29863	Human farnesyl pyrophosphate synthetase mRNA	9e-015	182405	(M29863) farnesyl pyrophosphate synthetase [Homo sapiens]	0.005
249	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	3e-015	<NONE>	<NONE>	<NONE >

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
250	Z80150	H.sapiens CACNL1A4 gene, exons 41 and 42 > :: emb|A70716.1|A70716 Sequence 37 from Patent WO9813490	3e-015	3387914	(AF070550) cote1 [Homo sapiens]	3.5
251	U28049	Human TBX2 (TXB2) mRNA, complete cds.	4e-016	2501116	TBX2 PROTEIN (T-BOX PROTEIN 2) tbx gene [Mus musculus]	6e-009
252	U31629	Mus musculus C2C12 unknown mRNA, partial cds.	1e-017	3024998	HYPOTHETICAL HEART PROTEIN	3e-017
253	J05262	Human farnesyl pyrophosphate synthetase mRNA, complete cds.	1e-018	182405	(M29863) farnesyl pyrophosphate synthetase [Homo sapiens]	0.0001
254	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	5e-019	<NONE>	<NONE>	<NONE>
255	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	5e-019	3219984	HYPOTHETICAL PROTEIN MJ1597.1 region MJ1597.1 [Methanococcus jannaschii]	5.7

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
256	NM_004587 .1	Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1) mRNA > :: gb|AF006751| AF006751 Homo sapiens ES/130 mRNA, complete cds	2e-019	4759056	ribosome binding protein 1 (dog 180kD homolog) >gi|3299885 (AF006751) ES/130 [Homo sapiens]	0.004
257	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	5e-020	3462455	(U89915) junctional adhesion molecule [Mus musculus]	2e-005
258	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	5e-020	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	9e-025
259	NM_004587 .1	Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1) mRNA > :: gb|AF006751| AF006751 Homo sapiens ES/130 mRNA, complete cds	2e-020	4759056	ribosome binding protein 1 (dog 180kD homolog) >gi|3299885 (AF006751) ES/130 [Homo sapiens]	0.0008

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
260	AF051098	Mus musculus seven transmembrane domain orphan receptor mRNA, complete cds	2e-021	3858883	(U67056) myosin I heavy chain kinase [Acanthamoeba castellanii] >gi|4206769 (AF104910) myosin I heavy chain kinase [Acanthamoeba castellanii]	0.002
261	AF051098	Mus musculus seven transmembrane domain orphan receptor mRNA, complete cds	2e-021	3858883	(U67056) myosin I heavy chain kinase [Acanthamoeba castellanii] >gi|4206769 (AF104910) myosin I heavy chain kinase [Acanthamoeba castellanii]	0.001
262	M13519	Human N-acetyl-beta-glucosaminidase (HEXB) mRNA, 3' end.	2e-021	4504373	hexosaminidase B (beta polypeptide) >gi|123081|sp|P07686|HEXB_HUMAN BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR beta-N-acetylhexosaminidase (EC 3.2.1.52) beta chain - human >gi|386770 (M23294) beta-hexosaminidase beta-subunit [Homo sapiens]	2e-007

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
263	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	2e-022	<NONE>	<NONE>	<NONE>
264	AF147311.1	Homo sapiens full length insert cDNA clone YA82F10	2e-022	3875904	(Z70207) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65905 comes from this gene; cDNA EST EMBL:D65858 comes from this gene; cDNA EST EMBL:D69306 comes from this gene; cDNA EST EMBL:D65755 comes from this gen...	0.07
265	AF037088	Gorilla gorilla ribonuclease k6 precursor, gene, complete cds	9e-024	3914791	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi|2745752 (AF037082) ribonuclease k6 precursor	3e-019
266	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X	8e-024	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
		*				
267	AF037088	Gorilla gorilla ribonuclease k6 precursor, gene, complete cds	9e-025	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi|2745760 (AF037086) ribonuclease k6 precursor	4e-018
268	AF147311.1	Homo sapiens full length insert cDNA clone YA82F10	1e-026	131413	PULMONARY SURFACTANT-ASSOCIATED PROTEIN A PRECURSOR (SP-A) (PSP-A) (PSAP) precursor - rabbit >gi|165706 (J03542) apoprotein of surfactant [Oryctolagus cuniculus]	0.059
269	Z46786	D.melanogaster mRNA for acetyl-CoA synthetase	1e-027	1079042	acetyl-CoA synthetase - fruit fly	4e-025
270	NM_004039.1	Homo sapiens annexin II (lipocortin II) for lipocortin II, complete cds	4e-028	450448	(M33322) calpactin I heavy chain [Mus musculus]	0.1
271	X53064	Homo sapiens SPRR2A gene encoding small proline rich protein	1e-028	134846	SMALL PROLINE-RICH PROTEIN II rich protein [Homo sapiens]	0.005

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
272	M29863	Human farnesyl pyrophosphate synthetase mRNA	1e-028	4503685	farnesyl diphosphate synthase dimethylallyltransferase, geranyltranstransferase) bp313 to bp1374 is almost identical to human farnesyl pyrophosphate synthetase mRNA. [Homo sapiens]	2e-008
273	Z18950	H.sapiens genes for S100E calcium binding protein, CAPL, and S100D calcium binding protein EF-Hand patent US 5789248	5e-029	2493898	DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (DOPAMINE BETA-HYDROXYLASE) (DBH) 1.14.17.1) precursor - mouse >gi|260873|bbs|119249 621 aa] [Mus sp.]	1.4
274	M19481	Human follistatin gene, exon 6.	5e-030	<NONE>	<NONE>	<NONE>

Table 2

<table>
<tr><th></th><th>Nearest Neighbor (BlastN vs. Genbank)</th><th></th><th></th><th>Nearest Neighbor (BlastX vs. Non-Redundant Proteins)</th><th></th><th></th></tr>
<tr><td>275</td><td>AF007155</td><td>Homo sapiens clone 23763 unknown mRNA, partial cds</td><td>2e-032</td><td>4502641</td><td>chemokine (C-C) receptor 7 TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1) (EBI1) (BLR2) >gi|1082381|pir||B55735 lymphocyte-specific G-protein-coupled receptor EBI1 - human >gi|468316 (L3158</td><td>1.6</td></tr>
<tr><td>276</td><td>M99624</td><td>Human epidermal growth factor receptor-related gene, 5' end.</td><td>8e-034</td><td>294845</td><td>(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]</td><td>9e-014</td></tr>
<tr><td>277</td><td>U49082</td><td>Human transporter protein (g17) mRNA, complete cds</td><td>8e-035</td><td>1840045</td><td>(U49082) transporter protein [Homo sapiens]</td><td>1e-014</td></tr>
</table>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
278	D50369	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds	9e-036	3024781	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C PROTEIN) (COMPLEX III SUBUNIT VII) ubiquinone-binding protein [Homo sapiens]	0.0002
279	AF086313	Homo sapiens full length insert cDNA clone ZD52B10	9e-036	2832777	(AL021086) /prediction=(method:; comes from the 5' UTR [Drosophila melanogaster]	1e-039
280	NM_004074.1	Homo sapiens cytochrome c oxidase subunit VIII (COX8), nuclear gene encoding mitochondrial protein, mRNA > :: gb|J04823|HUMCOX8A Human cytochrome c oxidase subunit VIII (COX8) mRNA, complete cds.	1e-038	2499854	PROBABLE PEPTIDASE Y4SO >gi|2182630	2
281	AB024436.1	Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds	2e-041	3132900	(AF038662) beta-1,4-galactosyltransferase [Homo sapiens] beta-1,4-galactosyltransfe	4e-016

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
					galactosyltransferase IV [Homo sapiens]	
282	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	2e-043	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	3e-062
283	Z69650.1	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene	2e-044	1872200	(U22376) alternatively spliced product using exon 13A	1e-008
284	NM_003938.1	Homo sapiens adaptin, delta (ADTD) mRNA > :: gb|U91930|HSU91930 Homo sapiens AP-3 complex delta subunit mRNA, complete cds	2e-044	3478639	(AC005545) delta-adaptin, partial CDS [Homo sapiens]	3e-016
285	AF026029	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds	8e-045	1916930	(U88570) CREB-binding protein homolog [Drosophila melanogaster]	7.6
286	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	1e-045	73404	E2 protein - human papillomavirus type 5	0.11

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
287	U90918	Human clone 23654 mRNA sequence	1e-048	3877568	(Z70208) similar to collagen	0.042
288	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	1e-049	73404	E2 protein - human papillomavirus type 5	0.11
289	AL049258.1	Homo sapiens mRNA; cDNA DKFZp564E173 (from clone DKFZp564E173)	1e-050	<NONE>	<NONE>	<NONE >
290	AF022367	Homo sapiens beta-1,4-galactosyltransferase mRNA, complete cds	5e-051	3132900	(AF038662) beta-1,4-galactosyltransferase [Homo sapiens] beta-1,4-galactosyltransferase IV [Homo sapiens]	6e-019
291	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	7e-053	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-055
292	AF097709	Homo sapiens serine protease (PRSS11) mRNA, partial cds	8e-055	4506141	protease, serine, 11 (IGF binding) >gi|1513059|dbj|BAA13322| (D87258) serin protease with IGF-binding motif [Homo sapiens] protease, PRSS11 [Homo sapiens]	2e-017

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
293	U31629	Mus musculus C2C12 unknown mRNA, partial cds.	9e-057	3025215	HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III >gi|2146877|pir||S72572 probable ABC1 protein homolog - Caenorhabditis elegans protein (Swiss-Prot Acc: P27697) [Caenorhabditis elegans]	5e-033
294	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	8e-057	73404	E2 protein - human papillomavirus type 5	1.7
295	AF025439	Homo sapiens Opa-interacting protein OIP3 mRNA, partial cds	4e-059	<NONE>	<NONE>	<NONE>
296	M99624	Human epidermal growth factor receptor-related gene, 5' end.	1e-060	123364	SEGMENTATION PROTEIN EVEN-SKIPPED fly (Drosophila sp.) >gi|157387 (M14767) even-skipped gene [Drosophila melanogaster]	5.3
297	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	5e-061	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	7e-029
298	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	2e-062	2119133	ribosomal protein S17 - cat (fragment) musculus]	2e-015

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
299	M30702	Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).	2e-063	4502199	amphiregulin (schwannoma-derived growth factor) >gi|113754|sp|P15514|AMPR_HUMAN AMPHIREGULIN PRECURSOR (AR) (COLORECTUM CELL-DERIVED GROWTH FACTOR) (CRDGF) >gi|107391|pir||A34702 amphiregulin precursor - human >gi|178890 (M30703) amphiregulin [Homo sapien	0.0002
300	L38847	Mus musculus hepatoma transmembrane kinase ligand Sequence 1 from patent US 5624899	6e-064	3861228	(AJ235272) unknown [Rickettsia prowazekii]	2.9
301	L38847	Mus musculus hepatoma transmembrane kinase ligand Sequence 1 from patent US 5624899	6e-064	3861228	(AJ235272) unknown [Rickettsia prowazekii]	2.9
302	Z78141	M.musculus partial cochlear mRNA (clone 29C9)	8e-066	1490324	(Z78141) unknown [Mus musculus]	8e-019

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
303	X12650	Mus musculus gene for beta-tropomyosin	2e-072	833602	(X54277) cardiac tropomyosin [Coturnix coturnix]	7e-022
304	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	2e-084	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	5e-019
305	M13364	Rabbit calcium-dependent protease, small subunit mRNA, complete cds.	2e-084	115611	CALCIUM-DEPENDENT PROTEASE, SMALL NEUTRAL PROTEINASE) (CANP) >gi|108563|pir||A34466 calpain (EC 3.4.22.17) II light chain - bovine 3.4.22.17) [Bos taurus]	1e-058
306	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	3e-088	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	9e-028
307	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	5e-092	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	2e-035
308	X85992	M.musculus mRNA for semaphorin C	8e-097	2137756	semaphorin C - mouse (fragment) musculus]	2e-048

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
309	M24103	Bovine ADP/ATP translocase T2 mRNA, complete cds.	e-103	113463	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) >gi|86757|pir||S03894 ADP,ATP carrier protein T2 - human	2e-035
310	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-107	1216486	(U48852) HT protein [Cricetulus griseus]	3e-057
311	X76168	R.norvegicus mRNA for connexin 30.3	e-112	544118	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) >gi|481577|pir||S38891 connexin 30.3 - rat >gi|431204|emb|CAA53762| (X76168) connexin 30.3	1e-063
312	X76168	R.norvegicus mRNA for connexin 30.3	e-115	461864	GAP JUNCTION BETA-5 PROTEIN junction protein Cx30.3 - mouse >gi|192647 (M91443) connexin 30.3 [Mus musculus]	7e-064

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
313	AJ009634.1	Mus musculus fjx1 gene	e-137	4138203	(AJ009634) Fjx1 [Mus musculus]	5e-065
314	X76168	R.norvegicus mRNA for connexin 30.3	e-130	544118	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) >gi|481577|pir||S38891 connexin 30.3 - rat >gi|431204|emb|CAA53762| (X76168) connexin 30.3	2e-074

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
4	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
8	728115					
		_15,16 (Normal Colon vs. Colon Tumor)	0	7		6.62
		_16,17 (Colon Tumor vs. Colon Metastasis)	7	0	7.11	
9	372700					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	3	50		11.93
		_19,20 (Colon Tumor vs. Colon Tumor Metastasis)	8	0	5.98	
12	729832					
		_15,16 (Normal Colon vs. Colon Tumor)	0	11		10.41
		_16,17 (Colon Tumor vs. Colon Metastasis)	11	0	11.17	
13	505514					
		_23,24 (Normal Lung vs. Lung Tumor)	26	10	2.63	
17	549934					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	0	7.87	
		_16,17 (Colon Tumor vs. Colon Metastasis)	3	20		6.56
		_15,16 (Normal Colon vs. Colon Tumor)	11	3	3.88	
25	450399					

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		_15,16 (Normal Colon vs. Colon Tumor)	28	68		2.3
		_15,17 (Normal Colon vs. Colon Metastasis)	28	117		3.89
26	450982					
		_16,17 (Colon Tumor vs. Colon Metastasis)	14	32		2.25
28	379302					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	1	7.87	
43	817503					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	4	4.43	
48	830085					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	9		9.15
52	830931					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
55	819046					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	13		6.61
58	728115					
		_15,16 (Normal Colon vs. Colon Tumor)	0	7		6.62
		_16,17 (Colon Tumor vs. Colon Metastasis)	7	0	7.11	
65	553242					

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		_16,17 (Colon Tumor vs. Colon Metastasis)	0	6		5.91
71	820061					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	20		20.33
78	220584					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	1	12		8.59
80	549934					
		_16,17 (Colon Tumor vs. Colon Metastasis)	3	20		6.56
		_15,16 (Normal Colon vs. Colon Tumor)	11	3	3.88	
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	0	7.87	
86	819460					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	1	17.7	
95	551785					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
96	17092					
		_03,04 (Breast, High Metastatic Potential vs. Breast, Non-Metastatic)	0	25		25.62
99	745559					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	9		9.15

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
101	379879					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	9		9.15
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	13		9.3
107	268290					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	33	69		2.13
108	818043					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
114	450247					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	23	8	2.83	
115	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
116	587779					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
118	615617					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
121	818682					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	2	5.41	

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
123	484413					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
124	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
127	818682					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	2	5.41	
131	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
147	820061					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	20		20.33
153	375958					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	11		5.59
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	9		6.44
155	831049					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	11		11.18
157	553200					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
158	139677					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
159	139677					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
163	375958					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	9		6.44
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	11		5.59
168	831812					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
176	193373					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
177	400619					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	6	0	8.38	
178	831149					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
180	817503					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	4	4.43	

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
187	648679					
		_23,24 (Normal Lung vs. Lung Tumor)	11	1	11.11	
		_16,17 (Colon Tumor vs. Colon Metastasis)	79	0	80.23	
		_15,17 (Normal Colon vs. Colon Metastasis)	7	0	7.51	
		_15,16 (Normal Colon vs. Colon Tumor)	7	79		10.68
190	373928					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
195	373928					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
198	372700					
		_19,20 (Colon Tumor vs. Colon Tumor Metastasis)	8	0	5.98	
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	3	50		11.93
204	379105					
		_15,16 (Normal Colon vs. Colon Tumor)	0	8		7.57
205	831188					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	8		8.13
209	831812					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
213	831026					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	10		10.17
215	380207					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	8		5.72
216	819460					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	1	17.7	
224	819201					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
225	374826					
		_15,17 (Normal Colon vs. Colon Metastasis)	5	20		3.73
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	38	132		2.49
		_15,16 (Normal Colon vs. Colon Tumor)	5	18		3.41
231	553242					
		_16,17 (Colon Tumor vs. Colon Metastasis)	0	6		5.91
246	220584					
		_08;09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	1	12		8.59
248	819498					

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
253	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
256	831160					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	12		12.2
259	831160					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	12		12.2
262	373298					
		_15,17 (Normal Colon vs. Colon Metastasis)	126	42	3.22	
		_15,16 (Normal Colon vs. Colon Tumor)	126	59	2.26	
270	450262					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	8		8.13
271	484703					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	28	0	27.54	
272	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	

Table 4

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
273	406043					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
274	817500					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	18		9.15
275	818180					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	10		5.08
280	429009					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	1	7.87	
284	383021					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	3	12		4.07
289	831580					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
311	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
312	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
314	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
315	10154					
		_3,4 (Breast,High Metastatic Potential vs. Breast, Low Metastatic)	3	317		108.1

Table 7

Library No.	Clones	Library No.	Clones
es75	M00063947D:D01	es79	M00064003B:C10
	M00063158A:A01		M00064302A:D10
	M00063517A:A04		M00064309C:H09
	M00063520D:E11		M00064310D:F03
	M00063638C:G12		M00064322C:A10
	M00063642B:A08		M00064359B:H12
	M00063686B:E07		M00064390A:C05
	M00063689D:E12		M00064404A:B05
	M00063781B:B10		M00064404C:G05
	M00063826A:D03		M00064404D:A06
es76	M00063838B:G08	es80	M00064429D:B07
	M00063838B:G08		M00064446A:D11
	M00063841A:B09		M00064457D:C09
	M00063886A:B06		M00064476D:C04
	M00063910D:A12		M00064506A:C07
	M00063912A:D06		M00064514A:G10
	M00063920D:H05		M00064520A:F08
	M00063928A:G09		M00064579D:E11
	M00063934B:E04		M00064620C:D01
	M00063945A:C03		M00064624D:C09
es77	M00064032D:G04	es81	M00064633C:A03
	M00064046A:G02		M00064637B:F03
	M00064053C:G04		M00064690A:C04
	M00064053D:F02		M00064690A:C04
	M00064082A:A08		M00064714A:G03
	M00064089B:F09		M00064723D:H11
	M00064132B:B07		GKC10154-1
	M00064138A:F11		GKC10154-3
	M00064161B:G04		
	M00064175B:B09		
es78	M00064178C:C04		
	M00064179A:C04		
	M00064200D:E08		
	M00064248A:E02		
	M00064270B:B03		
	M00064271B:D03		
	M00063580C:A06		
	M00063594B:H07		
	M00064002C:F06		
	M00064002C:H09		

es82	M00063151A:G06	M00063852D:F07
	M00063151D:B10	M00063888D:D05
	M00063152C:B07	M00063888D:F02
	M00063156D:H10	M00063890A:F11
	M00063158A:E11	M00063890A:H04
	M00063158A:E11	M00063891A:F11
	M00063452A:F08	M00063892B:G02
	M00063453B:F08	M00063898A:A10
	M00063462D:D07	M00063915C:E01
	M00063463D:B05	M00063919C:E07
	M00063466C:C11	M00063920D:H02
	M00063467D:H07	M00063922B:A12
	M00063478C:D01	M00063925B:F04
	M00063482A:A08	M00063926A:H04
	M00063482A:F07	M00063931B:E10
	M00063485A:E05	M00063931B:F07
	M00063487C:C02	M00063932D:G08
	M00063514C:D03	M00063934C:C10
	M00063514C:E08	M00063938B:H07
	M00063515B:F06	M00063939C:D06
	M00063515B:H02	M00063939C:H01
	M00063518D:A01	M00063940D:F09
	M00063520D:D08	M00063940D:F09
	M00063604A:B11	M00063941B:C12
	M00063606C:B04	M00063943B:G12
	M00063610D:C11	M00063949D:A05
	M00063613D:C11	M00064021D:H01
	M00063617D:F09	M00064025D:E07
	M00063627C:F06	M00064025D:H12
	M00063636A:E01	M00064033C:C11
	M00063681B:C02	M00064033D:B01
	M00063682A:C04	M00063843B:D07
	M00063685A:C02	M00063848C:G11
	M00063774A:D09	M00063852B:D08
	M00063784A:H12	M00063818C:A09
	M00063784C:E10	M00063828A:H12
	M00063785C:F03	M00063828D:E05
	M00063795C:D09	M00063839A:F01
	M00063801B:D04	M00063841A:E08
	M00063804C:A11	
	M00063805D:E05	
	M00063807A:D12	
	M00063810C:E03	

es83	M00064043D:C09	M00063577C:C02
	M00064048C:G12	M00063578B:E02
	M00064053B:D09	M00063578C:A06
	M00064057C:H10	M00063580D:B06
	M00064059A:C11	M00063593A:D03
	M00064060B:D03	M00063600C:C09
	M00064079C:A10	M00063955C:F07
	M00064082D:D10	M00063955D:F05
	M00064083D:E05	M00063956A:F05
	M00064086C:E01	M00063957A:E02
	M00064090C:A02	M00063957A:E02
	M00064090D:D09	M00063967C:A12
	M00064105B:A03	M00063967D:G02
	M00064106C:G03	M00063968D:G08
	M00064113B:C04	M00063972C:E10
	M00064115B:E12	M00063978B:B06
	M00064119B:H10	M00063981D:A06
	M00064119C:D12	M00063990A:D05
	M00064122C:B06	M00063990A:D05
	M00064126C:C02	M00063997C:B12
	M00064126C:F12	M00063998C:E09
	M00064136C:D12	M00064000B:C03
	M00064144D:A07	M00064001A:B03
	M00064151B:C07	M00064005D:A08
	M00064159A:H03	M00064008A:B01
	M00064165A:B12	M00064009A:C01
	M00064171D:E05	M00064014D:H05
	M00064171D:E05	M00064018C:E07
	M00064172C:A02	M00064293D:B12
	M00064173B:E01	M00064294D:F01
	M00064176D:H10	M00063557D:C07
	M00064178B:A05	M00063559D:G03
	M00064178B:A05	M00063571B:G03
	M00064180A:G03	M00063575B:G02
	M00064186C:B03	M00063555B:D01
	M00064188B:G08	M00063533A:C12
	M00064194C:D02	M00063534C:A02
	M00064212D:E04	M00063538D:B01
	M00064260C:E05	M00063539C:C11
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	M00064481C:F03	M00064527A:H07
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	M00064514D:F11	M00064532D:G06
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	M00064517B:F10	M00064520A:E04
	M00064517C:F11	M00064524A:A09

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
15	21	Ascending colon	4.0	T3	G2	extending into subserosal adipose tissue	positive	3/8	N1	negative		MX	invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen
52	71	Ascending colon	9.0	T3	G3	Invasion through muscularis propria, subserosal involvement; ileocec. valve involvement	negative	0/12	N0	negative		M0	Hyperplastic polyp in appendix.
121	140	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving submucosa of urinary bladder	negative	0/34	N0	negative		M0	Perineural invasion; donut anastomosis negative. One tubulovillous and one tubular adenoma with no high

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
													grade dysplasia.
125	144	Cecum	6	T3	G2	Invasion through the muscularis propria into suserosal adipose tissue. Ileocecal junction.	negative	0/19	N0	negative		M0	patient history of metastatic melanoma
128	147	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into percolonic fat	positive	1/5	N1	negative		M0	
130	149	Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue	positive	10/24	N2	negative		M1	

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
133	152	Rectum	5.0	T3	G2	Invasion through muscularis propria into non-peritonealized pericolic tissue; gross configuration is annular.	negative	0/9	N0	negative		M0	Small separate tubular adenoma (0.4 cm)
141	160	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolonic adipose tissue, but not through serosa. Arising from tubular adenoma.	positive	7/21	N2	positive (Liver)	adenocarcinoma consistant with primary	M1	Perineural invasion identified adjacent to metastatic adenocarcinoma.

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
156	175	Hepatic flexure	3.8	T3	G2	Invasion through mucsularis propria into subserosa/pericolic adipose, no serosal involvement. Gross configuration annular.	positive	2/13	N1	negative		M0	Separate tubolovillous and tubular adenomas
228	247	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectoal adipose, and serosa	positive	1/8	N1	negative		MX	Hyperplastic polyps

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
264	283	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.	negative	0/10	N0	negative		M0	Tubulovillous adenoma with high grade dysplasia
266	285	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolonic adipose, extends to serosa.	negative	0/15	N1	positive (Mesenteric deposit)	0.4 cm, may represent lymph node completely replaced by tumor	MX	
268	287	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy	negative	0/12	N0	negative		M0	

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
278	297	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.	positive	7/10	N2	negative		M0	Descending colon polyps, no HGD or carcinoma identified..
295	314	Ascending colon	5.0	T3	G2	Invasion through muscularis propria into percolic adipose tissue.	negative	0/12	N0	negative		M0	Melanosis coli and diverticular disease.
339	358	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa	negative	0/6	N0	negative		M0	1 hyperplastic polyp identified
341	360	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	negative	0/4	N0	negative		MX	

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
356	375	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.	negative	0/4	N0	negative		M0	
360	412	Ascending colon	4.3	T3	G2	Invasion thru muscularis propria to pericolonic fat	positive	1/5	N1	negative		M0	Two mucosal polyps
392	444	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.	positive	1/6	N1	positive (Liver)	Macrovesicular and microvesicular steatosis	M1	Tumor arising at prior ileocolic surgical anastomosis.

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
393	445	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.	negative	0/21	N0	negative		M0	
413	465	Ascending colon	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.	negative	0/7	N0	positive (Liver)	adenocarcinoma in multiple slides	M1	rediagnosis of oophorectomy path to metastatic colon cancer.

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
505	383		7.5 cm max dim	T3	G2	Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved	positive	2/17	N1	positive (Liver)	moderately differentiated adenocarcinoma, consistant with primary	M1	Anatomical location of primary not notated in report. Evidence of chronic colitis.
517	395	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolonic fat.	positive	6/6	N2	negative		M0	No mention of distant met in report

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
534	553	Ascending colon	12	T3	G3	Invasion through the muscularis propria involving pericolic fat. Serosa free of tumor.	negative	0/8	N0	negative		M0	Omentum with fibrosis and fat necrosis. Small bowel with acute and chronic serositis, focal abscess and adhesions.
546	565	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending to serosa.	positive	6/12	N2	positive (Liver)	metastatic adenocarcinoma	M1	

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
577	596	Cecum	11.5	T3	G2	Invasion through the bowel wall, into suberosal adipose. Serosal surface free of tumor.	negative	0/58	N0	negative		M0	Appendix dilated and fibrotic, but not involved by tumor
695	714	Cecum	14	T3	G2	extending through bowel wall into serosal fat	negative	0/22	N0	negative		MX	tubular adenoma and hyperplstic polyps present, moderately differentiated adenoma with mucinous diferentiation (% not stated)
784	803	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues	positive	5/17	N2	positive (Liver)		M1	invasive poorly differentiated adenosquamous

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
													carcinoma
786	805	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface	negative	0/12	N0	positive (Liver)		M1	moderately differentiated invasive adenocarcinoma
791	810	Ascending colon	5.8	T3	G3	through the muscularis propria into pericolic fat	positive	13/25	N2	positive (Liver)		M1	poorly differentiated invasive colonic adenocarcinoma

Table 8 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymphnode Met	Regional Lymphnode Grade	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
888	908	Ascending colon	2.0	T2	G1	into muscularis propria	positive	3/21	N0	positive (Liver)		M1	well- to moderately-differentiated adenocarcinoma; this patient has tumors of the ascending colon and the sigmoid colon
889	909	Cecum	4.8	T3	G2	through muscularis propria int subserosal tissue	positive	1/4	N1	positive (Liver)		M1	moderately differentiated adenocarcinoma

We Claim:

1. An isolated polynucleotide comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS: 1-316.

2. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NOS:1-316, a degenerate variant of SEQ ID NOS:1-316, an antisense of SEQ ID NOS:1-316, and a complement of SEQ ID NOS:1-316.

3. A polynucleotide comprising a nucleotide sequence of an insert contained in a clone deposited as clone number xx of ATCC Deposit Number xx .

4. An isolated cDNA obtained by the process of amplification using a polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence of a sequence selected from the group consisting of SEQ ID NOS:1-316.

5. The isolated cDNA of claim 4, wherein amplification is by polymerase chain reaction (PCR) amplification.

6. An isolated recombinant host cell containing the polynucleotide according to claims 1, 2, 3, or 4.

7. An isolated vector comprising the polynucleotide according to claims 1, 2, 3, or 4.

8. A method for producing a polypeptide, the method comprising the steps of:

culturing a recombinant host cell containing the polynucleotide according to claims 1, 2, 3, or 4, said culturing being under conditions suitable for the expression of an encoded polypeptide;

recovering the polypeptide from the host cell culture.

9. An isolated polypeptide encoded by the polynucleotide according to claims 1, 2, 3, or 4.

10. An antibody that specifically binds the polypeptide of claim 9.

11. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene comprising an identifying sequence of at least one of SEQ ID NOS:1-316;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

12. A library of polynucleotides, wherein at least one of the polynucleotides comprises the sequence information of the polynucleotide according to claims 1, 2, 3, or 4

13. The library of claim 12, wherein the library is provided on a nucleic acid array.

14. The library of claim 12, wherein the library is provided in a computer-readable format.

15. A method of inhibiting tumor growth by modulating expression of a gene product, the gene product being encoded by a gene identified by a sequence selected from the group consisting of SEQ ID NOS:1-316.

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   1                                                                                   0
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   1                                                                                   0
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   1                                                                                   0
 241 AGACAACATTCAGTCTTATACTGCCACAGTCATTAGTGCTGCTAAAACATTGAAAAGTGGCCTGACAATGGTAGGGAAAG  320

   1                                                                                   0
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   1                                                                                   0
 401 CCTTTGGTCCCAGGCATCATCACAGTTATTGACACCGAAACCGTTGGAGAGGGCCAGGTGCTTGTGAGTGAGGATTCTGA  480

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   1                                                                                   0
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   1                                                                                   0
 641 GTCCACCATCTGTATACTCTTCACAGGCGAGAAACTGAAGCCAAAGTACAGGACATCTGCTTCAGCCATGACTGTCGCTG  720

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FIGURE 1A

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   1                                                                                    0
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   1                                                                                    0
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   1                                                                                    0
1601 GACCATAGTGGACAGGAAGATGAAGAATGGCTTTCCCAGGTTGAAATTGTAACACACACTGGACCCCATAGACGTCTGTG 1680

   1                                                                                    0
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   1                                                                                    0
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   1                                 TCGGAGCCCATGCGCAGCGGGGCGCGTTAGCTCGCGCTCTTCCTGACCCC   50
1841 CAGCCAGTCCGCTCTGACCCCGTCAGCATGCCAGGGTCATCCCGTCCAGTCTCTGATCGAAGGGGAGTTTCCACAGTGAT 1920
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 131 GCGGCACATGTCCTCCATGGAGCACACGGAGGAGGGCCTCCGGGAGCGACTTGCCGACGCCATGGCCGAGTCACCTAGCC  210
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     ** *****************     ***     *    * *    ** *

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FIGURE 1B

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  71 CCTCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGGTCCTACCCTTCAGTCTCTGCTCTTCCTTCATCAACCACCTTCC  150
 161 CCTCCCCTGCTGGAGGAGGGGAGAAGCCCCGCTCTGGTCCTACCCTTCAGTCTCTGCTCTTCCTTCATCAACCACCTTCC  240
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 151 CCAAGCTTAGTGACAGCAGCCGCCCATCCTACCTGGATGGAGAAGAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCT  230
 241 CCAAGCTTAGTGACAGCAGCCGCCCATCCTACCTGGATGGAGAAGAGACCCTTCTCCAAGCACCTCAGCGCACTTGCCCT  320
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 231 CTGCCACACCTGTCGGTGGAGGCTGTGGCCAGGAGAGACTGTAGAAGCTCGGTCCCTGTGTATGTTTGCA SEQ ID NO:316  300
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 301                                                                                   300
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 301                                                                                   300
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 301                                                                                   300
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FIGURE 2

SEQUENCE LISTING

<110> Williams, Lewis T.
Escobedo, Jaime
Innis, Michael A.
Garcia, Pablo Dominiguez
Sudduth-Klinger, Julie
Reinhard, Christoph
He, Zhijun
Randazzo, Filippo
Kennedy, Giulia C.
Pot, David
Kassam, Altaf
Lamson, George
Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
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Labat, Ivan
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Garcia, Veronica
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<223> n = A,T,C or G

<400> 4
ggcacgagga gagggtggtg ggtccctgag ttggtggaaa gggatagagn nnnnnnnnnn       60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nngagtagag gatgcctggt atgaggcaat      300
atttgggata gggaagggaa gcttgggatt ttagctacgt agagacactt gaaaattgga      360
gggaggaaag gagtgggtgg ctttggagn                                        389

<210> 5
<211> 279
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(279)
<223> n = A,T,C or G

<400> 5
cctctcccct tggaacccaa agaggaacgg ggccgaactt tataaacttt aggcaagggc       60
aaagggcgtg nnnnnnnnnn nnggggccaa ggggcatttc ccaagcgatt aaaatttggg      120
aacctttggt tacaaaaatt gcggggaaaa tttatttcgg gagcaatttt ccctttaaaa      180
atttgagaat tcttacccgg agagtgtgac ataatttaag gcgcctctgc ccaaagaggc      240
catgtgcgtg aggggaatac cgcgtttaat tatcacaaa                             279

<210> 6
<211> 388
<212> DNA
<213> Homo sapiens

<400> 6
ggcacgaggc agaggcctcc ctgcactggt cctggcctca ctcttttccc tgacccttgg       60
ggcccagggc catggaggga cccttaggag ttcaatgaga gagaccatga ggccactggg      120
ctttcccctt cccaggcctc ctgggtgcca ccccttacg ttattcttgg gcctctaata       180
agtgtcccac aggtgcctgg ccaggcccac ctgctgcaga tgtggtctgt gtgtgtgcat      240
```

gtgtgggtgt gtgtgggcac aggtgtgagt gtgtgagcaa cagtacccca ttccagtcgt 300
ttcctgctgt gactaagtca gcaacacagt tcctctgaca tgggccttgg ctgtgcttct 360
ttgggggtga agagattgcg gaggaagt 388

<210> 7
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(410)
<223> n = A,T,C or G

<400> 7
ggcacgaggg gaagtcgcgc atgcgcgagt gtacgcgttg ccggcgaaga ggggagcctg 60
acgactcgga aatttgaata ccacagtagc atggagtgtg acctcatgga gactgacatc 120
ttggagtcgt tggaagatct aggttacaag ggcccattgt tggaagatgg agcgctctct 180
caggcagtct ctgctggagc cagttccccc gagtttacca aactctgtgc ttggctggtg 240
tctgaattaa gagtgctctg taaactagag gaaaacgtgc aagcaactaa cagtccgagt 300
gaagctgaag aattccagct tgaggtgagt gggctactag gggagatgaa ctgcccgtat 360
ctttcactga catctgnnga tgtgaccaag cgccttctca ttcagaaaaa 410

<210> 8
<211> 229
<212> DNA
<213> Homo sapiens

<400> 8
ctaacaaaaa acactaaaaa aaaataaaag aaattaattg aaactgacct aactcgtggc 60
agggggaact cggctataag acccacaaac cctgctgact cataacaaac tgagttgtaa 120
gacattcatc gccgcgatat ccttgagtaa agaatgaact ctggaagccc acccacggac 180
aatgcacctt cacaaagatt ctgcactaat ctgagtgaag gtctttggt 229

<210> 9
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

<400> 9
ggcacgagag tagttgggaa atcttttata aatccaccta ttactaccta ttggtagggg 60
agattaaatt tctacaggta tggagagtcg gcttgactac actgtgtgga gcaagtttta 120
aagaagcaaa ggtatagcag ttccaagtan nnnnnnnnnn nnnnnagacc aaactctaga 180
tcttgcccaa aatggacggc cgcggcattt aaatgaagaa agatttattt ttcctttttt 240
cttttaagaa aaattttttt aaaaaatttt gattnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn 380

<210> 10
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 10
cacacacaca catccactct ctctttttgc tctcttctca cacacacata tctcccttac 60
tcacacactc tctctcacac accccctctt tcttttcccc cgcactttct ttctctcacg 120
cgcgcgcgca ctcactctct tttttcttct ctctctcact ctctctctcc gcgcgctctc 180
tcacacgctt tatatctctc tctctgaggg acttctctct cctctcactc ttattttttt 240
gttgtgtttt atagcgtctc tctcttccct nnnnnnnnnn ntctatatat acagagagag 300
atctctctgc tctctcc 317

<210> 11
<211> 391
<212> DNA
<213> Homo sapiens

<400> 11
ggcacgagag aattagctga aacccaccaa gagctgcata gagcacgttt agctagagta 60
ggagtttgca gtgctcatat gggaaatgct gctgctatac ttttaggaat ttctgagtgc 120
aatttagaaa catctagcac acttgaaaca ctgcgtatca ttttcctcac tcatgaatat 180
agtcatcaga attcataaat agtttacctg agccctttaa caacctcaaa taggccatat 240
ttctctctct ggttgatggc atggacccta caggaaaaac cacaccttac cgcttctgac 300
cagcatcact acaaaaagga gtgctgaagc caatcaccat gtaagcaaga taaaagcaaa 360
gggggtcttg cctgcccatc tctgttccat a 391

<210> 12
<211> 280
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(280)
<223> n = A,T,C or G

<400> 12
tgtgcgcgcc cccccggggc gctctctctc tacactcgtg cgctcccccc tctgtctgtc 60
tctctctcta gagtcacggt ctcctacacg gcgcgcacat gcgaggggca ctnnnnnnnn 120
nnngctcnnn nnnnnnnnnn nnnnnnnnnn cgnnnnnnnn nnnnnnntcc cttgtatact 180
ctctgtgtgc gcggggacan nnnnnnnnnn nngtgcgcgc gcgagagcgc gcgcgccaca 240
caagagagag cgcgccctnn nnnnnnnnnn naccgcgaac 280

<210> 13
<211> 311
<212> DNA
<213> Homo sapiens

<400> 13
cgctttttttg ggaacccaaa ccttttttgg ctggccggaa aaaatttcca cgggaagggt 60
aaaggggttt attaattttt ttggcaaaac aggggttaag aaaccttccc tcccggccta 120
agggtgggct aggctttgga aaggctaaaa gggggaaatt tctggccctt gttccaaggg 180
aaacatgggc tagggggaaa ccccaccccct tcagggccct ttaaaagggc ccccaaaaaa 240
agaacccctt tattaagggt taaaaaaggt taaaaaaggt gggaacctca tgggccaagg 300
caaatttttg t 311

<210> 14
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

<400> 14

ggcacgaggt cttttctgcc cacatctcac acaattgagg tgtctgaaca agcttgggga 60
gggtctataa ggggtaggct cnnnnnnnnn nnncccattt ggaaagggcg ttttgccaac 120
ccaagggctt ttttaagccg atttttnnnn nnnnnnccgg acttggtaat tggcttttgg 180
ctttttaaag cccaaaaaat aataattaag gggcccaaaa taaggaaggg caaaaaaagc 240
ctttactccc cctgcctttc aaaaagaaaa ggaaaaaccg gcccccccctt aataattggc 300
accccctaaaa aaagggggttt taaaaaaagc caaaaacaaa agggcctgga aaaaaatttt 360
gactttttttt aacccggaac ctgggaa 387

<210> 15
<211> 273
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(273)
<223> n = A,T,C or G

<400> 15
ctgtctctct ctctcccccc ctctccctcc cgcgcgcgca cgctctttca tctctctctc 60
tacagacagg ggggggtgtt ctctctccct ctcgagaggg accgcttttt ttttctcccc 120
ctctctcaca ctcggggtgt gcgcgctccc tttgggggct tttctatagg gcgcgctcta 180
aagaaagccc gcctttctcc tctgggtgcc tcctcccaca cccgggtttt ctccccccgct 240
gtttttgaag aaactcctcc tggtctcctt atn 273

<210> 16
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(283)
<223> n = A,T,C or G

<400> 16
ctctctctct ggcccccccc ctctctttac acacactttc tctcctctct ctcgctctct 60
cttttttttt ctctctcccc tcgctctctc tgtgtgtctc tatctcgtgt ctctctctgc 120
gtgtccctca cacacactcg cgcgagagat ctctctctat atctctcctt tgtctgtgtc 180
tctctctcgc gcgcccacac atctatatat ttttgcgcgc acacgcgaga gtgtgtccct 240
ctctctctct gcacnnnnnn nnnnnnnnnn cacacccctcc ccc 283

<210> 17
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 17
ggcacgagat gactccttcc ttaaaatcca gctcaaatct cccccctttt ggtggctttc 60
tctgacactc catcataaag ctaattgttt aagtatgatc cagtggcaca gtttattcct 120
acttcataac ttttatctca ctatgttgta agatattagg tatgtttctt ctactaccag 180
taattttcaa agagttaagg aagaaggata gaagacagca gtataggtga atgtgtgcat 240
gtgttnnnnn nnnnnnnngc catattggcc aaaatttttg gactggctgg taaaacaaag 300
gcttttcaaa ttttcaaata cctttaaaaa aaacctggaa attgttttgt nnnnnnnnnn 360
cgcccaaaaa aaaattttgg gcctgggggg ga 392

<210> 18
<211> 385

<212> DNA
<213> Homo sapiens

<400> 18
ggcacgaggc agaggcctcc ctgcactggt cctggcctca ctcttttccc tgacccttgg 60
ggcccagggc catggaggga cccttaggag ttcaatgaga gagaccatga ggccactggg 120
ctttcccctt cccaggcctc ctgggtgcca ccccсttacg ttattcttgg gcctctaata 180
agtgtcccac aggtgcctgg ccaggcccac ctgctgcaga tgtggtctgt gtgtgtgcat 240
gtgtgggtgt gtgtgggcac aggcgtgagt gtgtgagcaa cagtacccca ttccagtcgt 300
ttcctgctgt gactaagtca gcaacacagt tcctctgaca tgggccttgg ctgtgcttct 360
ttgggggtga agagattgct gaggc 385

<210> 19
<211> 383
<212> DNA
<213> Homo sapiens

<400> 19
gaaggcttgc ggagagaaaa ccctggagcc atcttcatag gaagaggaaa ggaaactgta 60
tgacaggaga atgaatcaag tttggggctc aaggtgccgg ccactgggaa aaacagctgc 120
cccgagttgc aaaactctgg gtcctatatg tataaactat gccctgagga aggaatctca 180
ggcgtatctt aggagaaaat gttctagctt gggaaacaaa cacaacagga ccgtgaatcc 240
aaatatttca agtgggttta gaggactgga gttctaaacg ctgcttttac tgtaagtgat 300
cacgccccgg aatgtgctga agaaaggaaa atgagccagt atcggcgagg actatgggca 360
aggaaaacga gagtgtgcga tgt 383

<210> 20
<211> 313
<212> DNA
<213> Homo sapiens

<400> 20
ctctccccсg cgctcttgag atatgcgcgc cccttttttc ttctacacgg ggggggcgc 60
gcctcttttt ctcgcgcgcc cccctctctc tcttttgtgc gcacgcgcgc gcgcgggggg 120
gttctttttt tgtgcggaga gagagtctgt ctcaggggtt tttttgtttt ctttcacgac 180
acacactttc tcccctgtgc atgtgttttg atgctctctc gagatatgtc tctctctctc 240
tgtgtgtgtg tgttgtgcgc ccccccctggg gagagcgctc ttctctctct cctcatatag 300
cgcgcgcgcg cga 313

<210> 21
<211> 396
<212> DNA
<213> Homo sapiens

<400> 21
ggcacgaggg gacccccttc acctctgtct agagagctgg gtagatcaga aacttggtga 60
cacctggcta gcacagagca ggctcacttg tcttggtccc actacccaga ttcctgcaga 120
cattgcaaac caaatgaagg ttgttgaatg accсctgtcc ccagccactt gttttgttat 180
catctgctct gcagtggaat gcctgtgtgt ttgagttcac tctgcatctg tatatttgag 240
tatagaaacc gagtcaagtg atcatgtgca tccagacaca ctgtgtcacc tgagccacag 300
agcaaatcac cttaacgatc tggaatgaaa ctgtgaccag tgccgccctg ggtggttctg 360
gagagactgc cgtcttcttg tttggccata ggtgcg 396

<210> 22
<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 22
tgaatatcag ggccctgaac atctctcacg cccgtcttct aaaagagaag aaaaaaacgc 60
gcgcgggctt tttctctctc tcagaggggt gaaacacaca atatctcggg gggccggggg 120
agagcccgct ctctctgcct gtaaaacaca cagaagtgcg ctcacgccct gcgcgggagc 180
ccacagactt ttttttaaaa caaaaagtat attggggtgt gttttaatct ccctctccgc 240
tcctagaggg ggggcgnnnn nnnnnnnnnn ntttttaaat agggggggccc gagtctcacc 300
caatagaagg 310

<210> 23
<211> 375
<212> DNA
<213> Homo sapiens

<400> 23
ggcacgagcc ggcgaagagg ggagcctgac gactcggaaa tttgaatacc acagtagcat 60
ggagtgtgac ctcatggaga ctgacatctt ggagtcgttg gaagatctag gttacaaggg 120
cccattgttg gaagatggag cgctctctca ggcagtctct gctggagcca gttcccccga 180
gtttaccaaa ctctgtgctt ggctggtgtc tgaattaaga gtgctctgta aactagagga 240
aaacgtgcaa gcaactaaca gtccgagtga agctgaagaa ttccagcttg aggtgagtgg 300
gctactaggg gagatgaact gcccgtatct ttcactgaca tctggggatg tgaccaagcg 360
ccttctcatt cagaa 375

<210> 24
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 24
gctccttctt cttnttgttg atcccatcga tccgaattcg gcacgagagc acctctgtgc 60
ctctctgaga gcactcacag ccaaaagtac acagctgccc ccaggctgag agtgcttgat 120
acacccttga atcccctctt atatgatgcc ccagcccagg agagataaaa gcatcagcac 180
catgagattc acctgcctct ggtcgtnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnact cttagacagc aaaaatgctt 360
tctcccagtc ttgttccctt gttctcagtt cccaccctgc ctggataact actgttcttg 420
gtttnnnnnn nnnnnnnnnn nnnnnnnnag tctcgtacca gattcataaa tcagccg 477

<210> 25
<211> 265
<212> DNA
<213> Homo sapiens

<400> 25
cgcgcggggg ggacccctct ctctctctct gttgcgcgcg ctctctcacc ccgtgtgtcg 60
cccccgatat tgtcagagag acccccctatt tttttctccc gccccacaca catctatgtg 120
taaaatgtgc gtgtctgtcg cgcacaccca cacactctcc ccgggggggtt tataaaatac 180
tcgcgcgcta tattttcgcc ccccttttttg tgtgtgggcg ccacaaaaac accacacgct 240
ctccccccctg tctctcgcgg gtgtt 265

<210> 26
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(388)
<223> n = A,T,C or G

<400> 26
ggcacgaggg aggctctttg ttatagatgc ttttgccccc ttaatacagc aatgagagca 60
ctgaccgaag aggcagccgt gactgtaaca cctccaatca cagcccagca agctgacaac 120
atagaaggac ccatagcctt gaagttctca cacctttgcc tggaagatca taacagttac 180
tgcatcaacg gtgcttgtgc attccaccat gagctagaga aagccatctg caggtgtcta 240
aaattgaaat cgccttacaa tgtctgttct ggagaaagac gaccactgtg aggcctttgt 300
gaagaatttt catcaaggca tctgtagaga tcagtgagcc caaaattaaa gttttcagat 360
gaaacaacaa aacttgtcaa gctgactn 388

<210> 27
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 27
ggcacgagag aggggctact ttagatgcaa aggggacaat tagaaggcta ctgaggtaat 60
ccggacaaaa agttgtaaat aaatcacggt ggcagtatgg tgaatagtgg aaggggtgta 120
tttgaagaaa ctggggaggc cgtgggagag gctggctagt gagaaatggg ccgaaggtga 180
aagcagctta ggggctggtt tccagttttc tggcactgca gactgggtag tgggaggtgg 240
ctttctcaag aggagaggtg agtgggaagg agcagggctg caggggaggt catggtcttg 300
ggagtggtgc tcagtctgac ttgcacatag gggagattat tttagatttc cgcaagaaaa 360
tgtccagcat gtagtcatat caatgnnnnn nnnnnnnnnn nnnnnnnnnn nntgagattt 420
acccaaaaag a 431

<210> 28
<211> 389
<212> DNA
<213> Homo sapiens

<400> 28
ggcacgagcc acccccaaga gtgtggccat ctggggccgt gtggtatttg ccactcagga 60
gacatgtccc tatgacatag cagtggtgag cctggaggag gacctggatg atgtccccat 120
ccctgtgccc gctgagcact tccatgaagg cgaggctgtg agtgtggtgg gctttggcgt 180
ctttggccag tcttgcgggc cctcggtgac ctcaggcatc ctttccgctg tggtgcaggt 240
gaatggcacg cccgtaatgc tgcagaccac gtgtgctgtg cacagcggct ccagtggggg 300
acccctcttc tccaaccact caggaaacct ccttggcata atcaccagca acacccggga 360
caataatacg gggccacct acccccacc 389

<210> 29
<211> 431
<212> DNA
<213> Homo sapiens

<400> 29
ggacgaggct ccagcgcact tttccaacac atcactgcat tatttgaatg caccatggca 60
gctattgtca ccttacttgg gagtgatcca gttggagctc tttatattcg gacatgtcga 120
gtattgatgc tttctgactg ggacacgatg ctttacaacc caaggccaga ttacggtacc 180
acagtgcact gtactcatga agccggctac ccactatata ccatcgtatt tatctattac 240
gcattctgct tggtattaat gatgctgctc cgacctcttc tggtgaagaa gaatgcatgt 300
gggttaggga aatctgatcg atataaaagt atttatgctg cactttactt cttcccaaat 360
gtaaccgtgc ttcaggcagc tgtgggaggc cttttatatt acgccttccc atacattata 420
ttagtggtat c 431

<210> 30
<211> 393
<212> DNA
<213> Homo sapiens

<400> 30
ggcacgagac tacacccgct tcgatgactg gtacctgtgg gttcagatgt acaaggggac 60
tgtgtccatg ccagtcttcc agtccttgga ggcctactgg cctggtcttc agagcctcat 120
tggagacatt gacaatgcca tgaggacctt cctcaactac tacactgtat ggaagcagtt 180
tgggggctc ccggaattct acaacattcc tcagggatac acagtggaga agcgagaggg 240
ctacccactt cggccagaac ttattgaaag cgcaatgtac ctctaccgtg ccacggggga 300
tcccaccctc ctagaactcg gaagagatgc tgtggaatcc attgaaaaaa tcagcaaggt 360
ggagtgcgga tttgcaacaa tcaaagatct gcg 393

<210> 31
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(459)
<223> n = A,T,C or G

<400> 31
gcaatcgcat tgtctttttg aggatnnnat naatgtcaat tcggcacgag ctttgtggat 60
gtttccagct gccatcgtca cccttctgtc tgctccctgg accagcttca ggacttgaag 120
gccctcgtgg ctgagatcat cacacatttg caggggctgc agagggactt atctctagca 180
gtctcctaca gcaggctcca ttcctcagac tggaatctgt gtactgtatt tgggatcctc 240
ctgggctatc ctgttcccta tacctttcac ctgaaccagg gagatgacaa ctgcttagct 300
ctgactccac tacgagtatt cactgcccgg atctcatggt tgctaggtca acccccaatc 360
ctgctctatt cttttagtgt cccagagagt ttgttcccac gcctgaggga cattctgaac 420
acctgggaga aagacctcag aacccgattt atgactcac 459

<210> 32
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(445)
<223> n = A,T,C or G

<400> 32
ggcacgagat ggagagcacc tctgtgcctc tctgagagca ctcacagcca aaagtacaca 60
gctgccccca ggctgagagt gcttgataca cccttgaatc cctcttata tgatgcccca 120
gcccaggaga gataaaagca tcagcaccat gagattcacc tgcctctggt cgtnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnactctt agacagcaaa aatgctnttc tccagtcttt gttccttggt ctcaaggtcc 360
acccttgctg gataactact ggtcttgggt tcctggggta aagatggaac ttgagtaagc 420
tcgacccaaa tccaaaatca atccg 445

<210> 33
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(429)
<223> n = A,T,C or G

<400> 33
ggcacgagcg cctgccctgc atcagggaga catgtcagct gaggagtaat tgaccagatt 60
tctgctttag aaatatggca gtggaggcag gagatggcat ctgaggccca ggctggggag 120
aagggtgctg ggatgagaac ctggagttca gaccagggaa gggatgagag cctaagaaga 180

ggagctctca ccctgagaca ggctggtgca ggagtctgct cgatccaggc ctgggtccct 240
ggttccctct gagcttggga ggactatgtg agacagaaca ggaccagggg cctgcattcc 300
cccttgtatt attcatcnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnna 420
tgatggccc 429

<210> 34
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 34
gttctgtggg aatagagggt ccctggtgac agggcagggc tagatctgga gcctgcactt 60
ggcctgtgac atactgtctt gtttctgaga atcctcccct acttctctag ttaatctcca 120
gagacttctg tgactactta atcacaaagg aaattttcag gaatattatc aaatactatt 180
ttagaaaaaa aaagagaagg gatttgaatg ttttcagttc agtttagnta tcnnnnnnnn 240
nnnnnnnccc caaacttcaa aatggaggcc ccccctcct ttaaccccc taaaaaaaat 300
tctgatgttt gaggtttggt tgccaattaa ccaaaccccc aaaaaaaaag ggggttaaac 360
cccattggaa agttttccta attttggggg gtgccctttg aggtggaccc ggttccctgc 420
cctgggaaag gccccaaag 439

<210> 35
<211> 440
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(440)
<223> n = A,T,C or G

<400> 35
ggcacgaggt gaagtcctgg ttccagactc cccttttgc cgggacatga tggatctgtc 60
agctggtgcc tatagtccta gagagctaga gatggaggga aattcagatc atctaaaccc 120
ttcagccctt cactggacag aagaggaaac tgaggctcca tctgcatgac gttcccagag 180
tcacggcaca aattcatgga agaagcagca ggaaactcag ttctccagtc tgggtccaat 240
gtgtgtttta gaaatatctc cacagggtta atgactcaat ttttcatgca tgattgctag 300
taatgacaat catgttatgt ttgtttctgt agctttggaa atcactcctt ccacttgagt 360
ttcaggtccc aactgtccac acctgcagga gtgaggtttt gctgagactg ataaggcact 420
cacattntgt gggagttgaa 440

<210> 36
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(423)
<223> n = A,T,C or G

<400> 36
acgagcgcnn nncctgcatc agggagacat gtcagctgag gagtaattga ccagatttct 60
gctttagaaa tatggcagtg gaggcaggag atggcatctg aggcccaggc tggggagaag 120
ggtgctggga tgagaacctg gagttcagac cagggaaggg atgagagcct aagaagagga 180
gctctcaccc tgagacaggc tggtgcagga gtctgctcga tccaggcctg ggtccctggt 240
tccctctgag cttgggagga ctatgtgaga cagaacagga ccaggggcct gcattccccc 300
ttgtattatt catcnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnatga 420
tgg 423

<210> 37
<211> 424
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(424)
<223> n = A,T,C or G

<400> 37
ggcttgtaga nctcggaggt tngcaagaat cgcattcggc acgagctggg acacagtgng 60
ctctcttata tttgttgctg gaataaatga atgaactaag gcagtcttgt agggatttac 120
tgttaaccac catgggaaaa ttaaataaat gcggggaagg aaaacgttct aaaattagaa 180
gactactttc tactctcagc ttctgattcc ctctgagcta agaaccagac agccttaggc 240
tggtaactcc tataagctgg tcctcctccc atgctgaccc catctttact gtacaattca 300
cttttcatgg actgaaggca ccaccaagat agatccagga gtgacaactc cagtgtaggt 360
gtccactgtt cccttaatct ctgtcctgct ccaagtataa ataaatcggg gccatttcct 420
taga 424

<210> 38
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(434)
<223> n = A,T,C or G

<400> 38
ggcacgaggt acacagctgc ccccaggctg agagtgcttg atacaccctt gaatcccctc 60
ttatatgatg ccccagccca ggagagataa aagcatcagc accatgagat tcacctgcct 120
ctggtcgtnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnna ctcttagaca gcaaaaatgc tttctcccag tcttgttccc 300
ttgttctcag ttcccaccct gcctggataa ctactgttct tggtttnnnn nnnnnnnnnn 360
nnnnnnnnnn agtctcgtac cagattcaaa aatcagtcaa ctacttcaaa aacaatgaca 420
tgctggctac ttaa 434

<210> 39
<211> 428
<212> DNA
<213> Homo sapiens

<400> 39
ggcacgagct ttgtggatgt ttccagctgc cagcgtcacc cttctgtctg ctccctggac 60
cagcttcagg acttgaaggc cctcgtggct gagatcatca cacatttgca ggggctgcag 120
agggacttat ctctagcagt ctcctacagc aggctccatt cctcagactg gaatctgtgt 180
actgtatttg ggatcctcct gggctatcct gttccctata cctttcacct gaaccaggga 240
gatgacaact gcttagctct gactccacta cgagtattca ctgcccggat ctcatggttg 300
ctaggtcaac cccaatcct gctctattct tttagtgtcc cagagagttt gttcccaggc 360
ctgagggaca ttctaaacac ctgggagaag gacctcagaa cccgatttag gactcagaat 420
gactttgc 428

<210> 40
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(429)
<223> n = A,T,C or G

<400> 40
ggcacgagtg gagagcacct ctgtgcctct ctgagagcac tcacagccaa aagtacacag 60
ctgcccccag gctgagagtg cttgatacac ccttgaatcc cctcttatat gatgccccag 120
cccaggagag ataaaagcat cagcaccatg agattcacct gcctctggtc gttagggaac 180
aatggaggcc tgcgatttgg agttaaactc tcagtgatct ctgtgttgac aacaccaaag 240
ctagaggaat ccagtaggat gtgggcatgg ttttcccgga aggctgactg agcagttctg 300
caaatgtttg caagtacagg gcagaatttc atccagcctc agaaccttga gccaagactc 360
agcatcagca aagccaaaag tttcattttc ttgactgtgg gagtgctagt cccaaccttt 420
agatggccn 429

<210> 41
<211> 430
<212> DNA
<213> Homo sapiens

<400> 41
actctgcaaa cagctacttg tgctgattgc aggagaccca taaattcgaa cgaggaacaa 60
ccgagacctg aaggggctga cgaacgcgat ttctgataag tatggggtcc ctgaagagaa 120
catttaccaa gcctacaata aatgcacgcg aggaatctta tgcaacatgg acaacaacat 180
cattcagcat tacagcaacc acgtcgcctt cctgctggac atggcggagc tggacggcaa 240
aattcagatc atccttaagg agctggaagg cctctcgagc atacaaaccc tcacgacctg 300
catggggcca gcagggacgt ggccccacgc cacacacaac ctctccacat gcctcaacgc 360
tgttacttga atgccttccc tgagggaaga ggcccttgag tcacagaccc acagacgtca 420
ggaccatggg 430

<210> 42
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(437)
<223> n = A,T,C or G

<400> 42
ggcacgaggc gccctctgcc cccctcagag ggtctctcct ctcgaccccc aaattccccc 60
agcatctcaa tcccttgcat ggggagcaag gcctcgagcc cccatggttt gggctccccg 120
ctggtggctt ctccaagact ggagaagcgg ctgggaggcc tggccccaca gcgggggcagc 180
aggatctctg tgctgtcagc cagcccagtg tctgatgtca gctatatgtt tggaagcagc 240
cagtccctcc tgcactccag caactccagc catcagtcat cttccagatc cttggaaagt 300
ccagccaact cttcctccag cctccacagc cttggctcag tgtccctgtg tacaagaccc 360
agtgacttcc aggctcccag aaaccccacc ctaaccatgg gccaacccag aacaccccac 420
tctccaccac tgggcan 437

<210> 43
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(432)
<223> n = A,T,C or G

<400> 43
ggnncagtga ccaccaggac ctggtgtctg tgcacatcta catcacccag ctggctgaga 60
agttcgacct caggaccact atgctgtaca tctgtgagcg gcacttccag aaggttctga 120

accggagtct attcacaggc ctgcgctcca tcacccactt tggccgtccc ccctttgagc 180
ccttcttcaa ctccctgcag gaggtccacc cccaggtccg gaagatcggg gtgtttagct 240
gtggcccccc tggcatgacc aagaatgtgg aaaaggcctg tcagctcatc aacaggcagg 300
accggactca cttctcccac cattatgaga acttctaggc cccttcccgg gggttctgcc 360
cactgtccag ttgagcagag gtttgagccc acacctcacc tctgttcttc ctatttctgg 420
ctgcctcagc cc 432

<210> 44
<211> 436
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(436)
<223> n = A,T,C or G

<400> 44
ggcacgagcc gaggcgcgcg tgttccgtgg ccgcttccag ggccgcgcgg cggtgatcaa 60
gcaccgcttc cccaagggct accggcaccc ggcgctggag gcgcggcttg gcagacggcg 120
gacggtgcag gaggcccggg cgctcctccg ctgtcgccgc gctggaatat ctgccccagt 180
tgtctttttt gtggactatg cttccaactg cttatatatg gaagaaattg aaggctcagt 240
gactgttcga gattatattc agtccactat ggagactgaa aaaactcccc agggtctctc 300
caacttagcc aagacaattg ggcaggtttt ggctcgaatg cacgatgaag acctcattca 360
tggtgatctc accacctcca acatgctcct gaaacccccc cttgaacagc tgaacattgt 420
gctcatagac tntggg 436

<210> 45
<211> 300
<212> DNA
<213> Homo sapiens

<400> 45
tctctctctc tctctctcac agacactttt accccatata tacacataaa atgtgtgcgc 60
gagagagaga gagccctctc gctctatata tatccccgcg gggggagat aaaaatatat 120
atccccacac tttatagggc gggctccccc ctctatcctg tgtgtagaga gaaatatata 180
tatatctgtg gggggagaga gagatctctc acccccccgc acacgcgagc tctttcttaa 240
gatgtgtgag cgccccccc ctgtttttgt aaaaaagaga ggggtatata tattgggggg 300

<210> 46
<211> 191
<212> DNA
<213> Homo sapiens

<400> 46
caaaacaaaa ccatgttccc actggtgatg cctgtctgac acgttttggt atttagtagg 60
aaatgaaggg tcttcaagct tcgagagaac cttcaaaatt gtcacaattg ctgaaaacag 120
aatgaatcgg gaacattatc tcaatatttt gcataataga caacaccaca gtgttttggt 180
tccctgacct g 191

<210> 47
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(302)
<223> n = A,T,C or G

<400> 47
gcccgggcgt gtgtgtatgt gtgtacacgc ccccgtgggc tctctgtcgc atcttgnnnn 60
nnnnnnnnnn nnnnnnnnnn nntgtannnn nnnnnncaca tagcgcgcgc gctcgcgcgc 120

acggagctat agagacacca ctctctctct gagatacacg cgcgcgcaca cactctgcgc 180
gcgcgcgctc ttctttgtct cgcgcgcgcg cccgctatgt ggagggtata tgtgggggaa 240
aatagcgagg tgtgcgcgca cccgcgcacg cgcgctctat atctctatat cttcagcgcg 300
cg 302

<210> 48
<211> 411
<212> DNA
<213> Homo sapiens

<400> 48
ggcacgaggc ttgcggggca ttaggactag agggttggtg aaaattcaga cagaatgtaa 60
cttgacaaag agaagacagc aacaactgta acaattatct tatgaatatt tgcgaaactc 120
aaagggatct gattggtgac ctctgggctt tatcaaatta acatcacaac ttctagaaga 180
aagtcaacct tcatctttta caatagaaat catatgtttt gctaacccat tcctatttag 240
gctgaaaaca attaagagtt atgggtactt aaaaaaatca ttatgtttat aaaattagtg 300
atagaaggag catagtgttc tatacagtca cacacataca cttccttatt tcttttattt 360
aaactttgag taacatagca gtctatgttt gggtcagttt tccctttttt g 411

<210> 49
<211> 408
<212> DNA
<213> Homo sapiens

<400> 49
ggcacgaggc acacaaagcc aagggcatac cctatagagt aaagctgcag ccaccctgtg 60
tctcatgtgc agctgaaata gtgatctgct tctgtcactg tcacatagac agccctgcat 120
gccccctgtc tcacacagtt tgtaatgaag acagctcctt ctcatctttc cataagcctg 180
agatacaagt tcagggactc agcaatgcac tttaggactg agctaggagg caaatatctg 240
aagcttgcta tgctgttctt tccattcctt ttccctctga aacacacaaa ataccaaagg 300
aacttacgca tcacaccact gagtcctcta actaatcata tgtgctcaga cacagctcaa 360
gcacacccct tagttaagag agaacctcca tatacattaa tttttttc 408

<210> 50
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 50
agagaaacat ccactcgaat tcggcacgag gacagggcag ggctagatct tttttctgca 60
cttggcctgt gacatactgt ctggtgtctg agaatcctcc cctacttctc tagttaatct 120
ccagagactt ctgtgactac ttaatcacaa aggaaatttt caggaatatt atcaaatact 180
atttagaaa aaaaaagaga agggatttga atgttttcag ttcagtttag ttatcnnnnn 240
nnnnnnnnnn ncccaaactc aagtatggag gcccccccct ctttaaaccc accaaaaaaa 300
ttttttgggg ttcagggtgg gttggccaac tacccaaacc cccaaagaaa atgggggtta 360
accccttga aaaagttttc ttactttggg gggctgccct tgagccg 407

<210> 51
<211> 312
<212> DNA
<213> Homo sapiens

<400> 51
ccccggggc gctctctttt tttttccccc caagtgagag agccccgcgc gcgtctctct 60
ctcgcatttt ttcgacaccc cccttgtgtg gggcggggcg cgcgtctgtg tgtgatacac 120
agaatgtgcg tggtgtgtct gagagacact cttcgcgctt gtgtgtgaga cacgagactt 180
tctcttttta gggggcgggg ggggagtttt atgtgtgcca catgttttct gtgtataaaa 240
agagcgcaca gagtgttttt tatatctgtg agagagacct ctctgtatat atacacgctc 300

agaggggaga gg 312

<210> 52
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(420)
<223> n = A,T,C or G

<400> 52
acgagggnnn nnaagcaccg cgggtacccc atgagggcct acaagctggc caccctggcc 60
atgacccatc tcaacctgag ctacaatcag gacacacacc ctgccattaa tgatgttttg 120
tgggcctgtg cgcttagcca ctcccttggt aaaaatgagc ttgcagctat aatacctctg 180
gtggtcaaga gtgtcaagtg tgcaacggta ctgtcagaca ttttgcgcag atgcactctg 240
accactcctg gcatggtggg acttcatggg aggaggaact ctggtaagct catgtcactg 300
gacaaagccc ccttgaggca actcttggat gccacgatcg gggcctacat caacacaacg 360
cactcacggc tcacacacat cagtcctcgg cactatagtg agtttataga gttcctcagc 420

<210> 53
<211> 394
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(394)
<223> n = A,T,C or G

<400> 53
ggcacgaggt gtggatgaca gagcgagacc ctgcctcatn nnnnnnnnnn nnnnnnnnnc 60
ccccccnnnn nnnnnnnaaa aacccggttg ggccccggct gttctttagg gccctaaaaa 120
ttgccccaaa aaaaattggc cgggccctaa aaaaaccccg gtttttttggg gagaattcaa 180
aaaagggtcg gtnnnnnnnn nntttttaaa cttccaaccg gcctcagggg gaaaaaacct 240
ggaaaactca atgggggttg gaacaaaatc aatatttggt cctaccggaa agcgttaaga 300
ttttaaacca gtaaaaatgg ccaannnnnn nnnnnnnnnn nnnnaacagg gcccccgggg 360
taagggctaa aaattttcag atttgaacct tttt 394

<210> 54
<211> 390
<212> DNA
<213> Homo sapiens

<400> 54
ggcacgagat tttcttggca ataagcggac tctgggactc cggctcccta ccccaaactg 60
aagcgcttcc gtgaacaccc ccgtcctccg taggggggagg ggagcaggcg ggatcctggg 120
tccctcataa gcactttggt tttaccgcct gcaacctcac tgtgcccgcc ccgcaccatg 180
ccctagcccc aggtctagcc gggcccattg caggggggcag cacttggggg catctccggc 240
acttgggtgg gaccaaggag atgccaccat agacctttcc ctcgccttct tcctccctag 300
tccgggttcc attcttttca ccagcaccca tcgcccaagg ggtaccgagg gggggcaggg 360
ggtggtcaat tcaaacccaa cccccgctcg 390

<210> 55
<211> 280
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(280)
<223> n = A,T,C or G

<400> 55
tctctctctc tctctgcgcc cacacctctc tcannnnnnn nnngcacgtg tatatctnnn 60
nnnnnnnnnn tttttttttag agagacatct cgcgcgtgtc tctctttttc ccgcccgccg 120
ctcttttctc gcgcgcgcgc gcacccccccc tgtgtggggc gcgcgctctc ttttttttttg 180
tgcgcgcgan nnnnnnnnnt ctctctctgt ggcgnnnnnn nnnnnntctc ttattttata 240
ttttgggggg cggggggcct cccctccccc ctgtgtgcct 280

<210> 56
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(398)
<223> n = A,T,C or G

<400> 56
ggcacgaggt ccacctcagc tcagcaatct catgccggtt ggcaattagt cagcataagc 60
cgatgcctgc ccatcagttc tttactctga ggtgttagag tggaataaaa atataaatac 120
ttacnnnnnn nnnnnnnnca atacccaacc ccctcccatt nnnnnnnnnn nnngcccgcc 180
cccctaaaat tcatggagag gcctatttcg tagccagcca ctatataaac cctgctggtt 240
gggcggnnnn nnnnnnnngt gaagggggga aaaaaaagcc tttttttgaa aaaattagtc 300
atttttgct ttttttggac acattttgcg ggacaaagaa ccctgtaaaa ccccccctatt 360
cnnnnnnnnn nnnnnnaacc tcaacgaggg gggggcgg 398

<210> 57
<211> 386
<212> DNA
<213> Homo sapiens

<400> 57
ggcacgagat tttcttggca ataagcggac tctgggactc cggctcccta ccccaaactg 60
aagcgcttcc gtgaacaccc ccgtcctccg taggggggagg ggagcaggcg ggatcctggg 120
tccctcataa gcactttggt tttaccgcct gcaacctcac tgtgcccgcc ccgcaccatg 180
ccctagcccc aggtctagcc gggcccattg caggggggcag cacttggggg catctccggc 240
acttgggtgg gaccaaggag atgccaccat agacctttcc ctcgccttct tcctccctag 300
tccgggttcc attcttttca ccagcaccca tcgcccaagg ggtaccgagg gggggcaggg 360
gggggtcaag tccaggccca cccccg 386

<210> 58
<211> 202
<212> DNA
<213> Homo sapiens

<400> 58
cactttttct atatgaatat cttggccgta tcatagactc aaaaaagaaa ttatgcaagt 60
tctttctgcc cccacctgcg ccaggggaga agtttacctt cgggaactcc agagttaaag 120
cagttgtggt gataattttt tatgctgaac acaccacgat ataaaaaaca acattcacgt 180
gctttatttt tgttatgtgt tt 202

<210> 59
<211> 394
<212> DNA
<213> Homo sapiens

<400> 59
ggcacgagtc tgcttctgtc actgtcacat agacagccct gcatgccccc tgtctcacac 60
agtttgtaat gaagacagct ccttctcatc tttccataag cctgagatac aagttcaggg 120
actcagcaat gcactttagg actgagctag gaggcaaata tctgaagctt gctatgctgt 180
tctttccatt cctttccct ctgaaacaca caaaatacca aaggaactta cgcaacacac 240
cactgagtcc tctaactaat catatgtgct cagacacagc tcaagcacac cccttagtta 300
agaaagaacc tccatataca ttaattttt tctgcctaaa aataaaattg cgttgtggca 360

gcaatttgga aactacagca aagtctccaa aaaa 394

<210> 60
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(246)
<223> n = A,T,C or G

<400> 60
cccctccttt tttaggcctg aatacaaagt agaagatcac tttccttcac tgtgctgaga 60
atttctagat actacagntc ttactcctct cttccctttg ttattcaggg tgaccaggat 120
ggcgggaggg gatctgtgtc actgtaggta ctgtgcccag gaaggctggg tgaagtgacc 180
atctaaattg caggatggtg aaattatccc catctgtcct aatgggctta cctcctcttt 240
gccttn 246

<210> 61
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 61
ggcacgagct tgcttccctc tcaccctctg cagtttccnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnncttc catatcgtaa actgccttgg aaccaattac cactaccagg 180
gagacaaact attgcttaga ggatgctgac aggagcagca tgccaaaatt ggaagaagga 240
gaaagtttaa gctctcctca ctatgagttt tcaagtataa aagacttttt cttccacgat 300
tttgagaaca actgaggact cttgtgacca ggacaacagg gaagcttgca gcaagatagc 360
tccaggttgg attcatgctt cgcaccccaa aggct 395

<210> 62
<211> 387
<212> DNA
<213> Homo sapiens

<400> 62
ggcacgaggc ttgcggggca ttatgactag agggttggtg aaaattcaga cagaatgtaa 60
cttgacaaag agaagacagc aacaactgta acaattatct tatgaatatt tgcgaaactc 120
aaagggatct gattggtgac ctctgggctt tatcaaatta acatcacaac ttctagaaga 180
aagtcaacct tcatctttta caatagaaat catatgtttt gctaacccat tcctatttag 240
gctgaaaaca attaagagtt atgggtactt aaaaaaatca ttatgtttat aaaattagtg 300
atagaaggag catagtgttc tatacagtca cacacataca cttccttatt tcttttattt 360
aaactttgag taacatagca gtctatg 387

<210> 63
<211> 401
<212> DNA
<213> Homo sapiens

<400> 63
ggcacgaggg aaactgtatg acaggagaat gaatcaggtt tggggctcaa ggtgccggcc 60
actgggaaaa acagctgccc cgagttgcaa aactctgggt cctatatgta taaactatgc 120
cctgaggaag gaatctcagg cgtatcttag gagaaaatgt tctagcttgg gaaacaaaca 180
caacaggacc gtgaatccaa atatttcaag tgggtttaga ggactggagt tctaaacgct 240
gcttttactg taagtgatca cgccccggaa tgtgctgaag aaaggaaaat gagccagtat 300

cggcgaggac tatgggcaag gaaaacgaga gtgtgcgatg tgtcaaagca agacatctgt 360
gtatagtaat ataaccaagt aatagatagt catagaatca a 401

<210> 64
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(274)
<223> n = A,T,C or G

<400> 64
cacgcacccg cctgtgtgtg tgcgcacaca cgctccctct ctctatagac agacacacac 60
tgcgcgctcg ctctctcttt tgtgtgcgct ctccgtgctc cccccctctc tctctttttt 120
ctctatatnn nnnnnnnnnn nnnnntctga gagctcgcgc gctcagcgtt ctattcacac 180
gcgcgttttt tttatatata tattttgtgc gcgccggggg gggcgcacac actctctctt 240
ttttgtgggt tcgctgtccg cgtccctcct tttg 274

<210> 65
<211> 279
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(279)
<223> n = A,T,C or G

<400> 65
cccttttttt tatacacccc cccttgtctg tctgttttgt gtgtctgccc cccttctctc 60
gttgtgatct ccctctctct tttttctccc cccgcgctct ctctctcttg cggggaggct 120
cacatacccc ctctctctct cttttttgaa ccacacattc cgtttctctt ttttttatct 180
ctacccctct ctcgtctgta ccccccacan nnnnnnnnnn nnnnnnnnnn nnnagagtag 240
agttgcgttc cccactctcc nnnnnnnnnn gtggggtgc 279

<210> 66
<211> 311
<212> DNA
<213> Homo sapiens

<400> 66
caaaacaaaa attaaaaatg acccccccttt aaaattttag ggggtccatt tttaaaaacc 60
ttaacagttt aaaggttctt ggtcagtttg gggaacccca ccttgagatg ggagcaaaaa 120
aggggatttt tttccaacat agcgagcggt ttagattttt tttgtcccgt tagagttgcc 180
ctgtgcacca cgccaaaacc tccagaggtc ttcttttttt acacaccctg tctgggggtg 240
tttctcagaa gattaacaca gcgcctgggg gtttaaggga ggggtgacct ccgcaggaca 300
ttatggggct t 311

<210> 67
<211> 386
<212> DNA
<213> Homo sapiens

<400> 67
ggcacgaggg aatctcaggc gtatcttatg agaaaatgtt ctagcttggg aaacaaacac 60
aacaggaccg tgaatccaaa tatttcaagt gggtttagag gactggagtt ctaaacgctg 120
cttttactgt aagtgatcac gccccggaat gtgctgaaga aaggaaaatg agccagtatc 180
ggcgaggact atgggcaagg aaaacgagag tgtgcgatgt gtcaaagcaa gacatctgtg 240
tatagtaata taatcaagta atagatagtc atagaatcaa gctgatgtat ttggcagggg 300
ccgcgggagg atgaggcaac tcccatcaga ttagaaagat gttaacactg taacaaaagt 360
ggggctcgag gaaggggaaa agcgca 386

<210> 68
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 68
ggcacgagga ggcagctgcc tttgtttgcc atggatgggt aggggctgca ctgagcagca 60
ccggtgttct tcatccggct gcaccccaa cagagctctt tcttccccag atccctttta 120
cagttggatt ctccctcttg gatctggctc tgccttagtc cgacctagag ggatcagctt 180
cgcccacgcc cactctcacc cggaaccttt catctcttat tgaagccttt taggcccatt 240
gggatgttca ttagaactct gaaaactaca gttctcccct ttatgaggac tgcaccacag 300
ctcgccctct cctgggttcc gcctgggtgc agagtgagcc catgggacag ccctctgaaa 360
ttatactgct tacaaccatg ctgagtctgc aaggan 396

<210> 69
<211> 397
<212> DNA
<213> Homo sapiens

<400> 69
ggcacgagtc ttagtcaaca tggacaacaa catcattcag cattacagca accacgtcgc 60
cttcctgctg gacatggggg agctggacgg caaaattcag atcatcctta aggagctgta 120
aggcctctcg agcatccaaa ccctcacgac ctgcaagggg ccagcaggga cgtggcccca 180
cgccacacac aacctctcca catgcctcag cgctgttact tgaatgcctt ccctgaggga 240
agaggccctt gagtcacaga cccacagacg tcagggccag ggagagacct aggggggtccc 300
ctggcctgga tccccatggt atgcttgaat ctgctccctg aacttcctgc cagtgcctcc 360
ccgtacccca aaacaatgtc accatggtta ccaccta 397

<210> 70
<211> 394
<212> DNA
<213> Homo sapiens

<400> 70
ggcacgagcc aaacctagca caaaacgggg ttcacaagcc atggtcgggg tccggggggg 60
acagaaatgg attttcttgg caataagcgg actctgggac tccggctccc taccccaaac 120
tgaagcgctt ccgtgaacac ccccgtcctc cgtaggggga ggggagcagg cgggatcctg 180
ggtccctcat aagcactttg gttttaccgc ctgcaacctc actgtgcccg ccccgcacca 240
tgccctagcc ccaggtctag ccgggcccat tgcagggggc agcacttggg ggcatctccg 300
gcacttgggt gggaccaagg agatgccacc atagaccttt ccctcgcctt cttcctccct 360
agtccgggtt ccattctttt caccagcacc catc 394

<210> 71
<211> 389
<212> DNA
<213> Homo sapiens

<400> 71
ggcacgagga aagttaagca tctacaggtt atggctttgg gagttccaat atcagtctat 60
cttttattca acgcaatgac agcactgacc gaagaggcag ccgtgactgt aacacctcca 120
atcacagccc agcaaggtaa ctggacagtt aacaaaacag aagctgacaa catagaagga 180
cccatagcct tgaagttctc acacctttgc ctggaagatc ataacagtta ctgcatcaac 240
ggtgcttgtg cattccacca tgagctagag aaagccatct gcaggtgtct aaaattgaaa 300
tcgccttaca atgtctgttc tggagaaaga cgaccactgt gaagcctttg tgaagaattt 360
tcatcaaggc atctgtagag atcagtgag 389

<210> 72
<211> 396

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 72
ggcacgaggc ctggccccac agcggggcag caggatctct gtgctgtcag ccagcccagt 60
gtctgatgtc agctatatgt ttggaagcag ccagtccctc ctgcactcca gcaactccag 120
ccatcagtca tcttccagat ccttggaaag tccagccaac tcttcctcca gcctccacag 180
ccttggctca gtgtccctgt gtacaagacc cagtgacttc caggctccca gaaaccccac 240
cctaaccatg ggccaaccca gaacacccca ctctccacca ctggccaaag aacatgccag 300
cagctgcccc ccatccatca ccaactccat ggtggacata cccattgtgc tgatcaacgg 360
ctgcccagaa ccagggtctt ctccacccca gcggan 396

<210> 73
<211> 386
<212> DNA
<213> Homo sapiens

<400> 73
ggcacgaggc cacctgttgc cctaacaccc tgtctgactc tctcccgctg cagcagccag 60
tccctcctgc actccagcaa ctccagccat cagtcatctt ccagatcctt ggaaagtcca 120
gccaactctt cctccagcct ccacagcctt ggctcagtgt ccctgtgtac aagacccagt 180
gacttccagg ctcccagaaa ccccacccta accatgggcc aacccagaac accccactct 240
ccaccactgg ccaaagaaca tgccagcagc tgccccccat ccatcaccaa ctccatggtg 300
gacataccca ttgtgctgat caacggctgc ccagaaccag ggtcttctcc accccagcgg 360
accccaggac accagaactc cgttca 386

<210> 74
<211> 390
<212> DNA
<213> Homo sapiens

<400> 74
ggcacgagct cagatccggg gactgcggat aaatggcctt aggccgcggg cagcgagatg 60
ttgcgttccg gtgtgggtgt gggtgtgcct ccgacggcgt ctcggtgcca gtgtcgaggt 120
tctttctgct tagctacccg gagccgacta cggaggagga cacctgagtt tacgtctctt 180
ccatctgctg ctcgcctcag ctgcctgggt ccccgacgag agccaggtga cacttaactc 240
cgccatctgc gttttgagca ctgttctcat aatggagttt cctgatttgg ggaagcattg 300
ttcagaaaag acttgcaagc agctagattt tcttccagta aaatgtgatg catgtaaaca 360
agatttctgt aaagatcatt ttccatacgg 390

<210> 75
<211> 399
<212> DNA
<213> Homo sapiens

<400> 75
ggcacgagaa atggccttag gccgcgggca gcgagatgtt gcgttccggt gtgggtgtgg 60
gtgtgcctcc gacggcgtct cggtgccagt gtcgaggttc tttctgctta gctacccgga 120
gccgactacg gaggaggaca cctgagttta cgtctcttcc atctgctgct cgcctcagct 180
gcctgggtcc ccgacgagag ccaggtgaca cttaactccg ccatctgcgt tttgagcact 240
gttctcataa tggagtttcc tgatttgggg aagcattgtt cagaaaagac ttgcaagcag 300
ctagattttc ttccagtaaa atgtgatgca tgtaaacaag atttctgtaa agatcatttt 360
ccatacgctg cacataagtg tccgtttgca ttccagaag 399

<210> 76
<211> 386
<212> DNA
<213> Homo sapiens

<400> 76
ggcacgagca aaggctcgca gcggccagaa acccggctcc gagcggcggc ggcccggctt 60
ccgctgcccg tgagctaagg acggtccgct ccctctatcc agctccgaat cctgatccag 120
gcgggggcca ggggcccctc gcctcccctc tgaggaccga agatgagctt cctcttcagc 180
agccgctctt ctaaaacatt cataccaaag aagaatatcc ctgatggatc tcatcagtat 240
gaactcttaa aacatgcaga agcaactcta ggaagaggga atctgagaca agctgctatg 300
ttgcctgagg gagaggatct caatgaatgg agtgctgcga acacctgggg attcttttac 360
cagcaacaac atggtttttg ggaact 386

<210> 77
<211> 395
<212> DNA
<213> Homo sapiens

<400> 77
ggcacgaggc catctccaaa tactgcggtt gttcagaagc tcttagtttg tgggctgtcc 60
ttgttatttc acttgaccat ctgtacaaca ttacctgtgg agtacaacat tgatgagcat 120
tttcaagcta cagcttcgtg gccaacaaag attatctatc tgtatatctc tcttttggct 180
gccagaccca aatactattt tgcatggacg ctagctgatg ccattaataa tgctgcaggc 240
tttggtttca gagggtatga cgaaaatgga gcagctcgct gggacttaat ttccaatttg 300
agaattcaac aaatagagat gtcaacaagt ttcaagatgt ttcttgataa ttggaatatt 360
cagacagctc tttggctcaa aagggtgtgt tatga 395

<210> 78
<211> 389
<212> DNA
<213> Homo sapiens

<400> 78
ggcacgaggc aggccgggat gttcgtcctg gtggaaatgg tggacaccgt ccggatcccc 60
ccttggcagt ttgagaggaa gctcaacgac tccattgccg aggagctgaa caagaagttg 120
gccaacaagg tcgtgtacaa cgtgggactc tgcatttgtc tgtttgatat caccaaactg 180
gaggatgcct atgtattccc tggggatggc gcatcacaca ccaaagtcca ttttcgctgc 240
gtggtgtttc atccattcct agatgagatt ctcattggga agatcaaagg ctgcagccca 300
gaaggagtgc acgtctctct aggcttcttc gatgacattc tcatcccccc agagtcactg 360
cagcagccag ccaagttcga cgaagcgga 389

<210> 79
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(365)
<223> n = A,T,C or G

<400> 79
ggcacgagaa aacatttcat cttgattttt attaaggtga tatgtatgtt acttaacagc 60
tgtataatac acatttgcat gcattaggaa gtttttttg ggttttattc atcctgtagt 120
gatgtatctg tgacctcaac gagtaggcac ttctgtactg tactggtttc ttaaagtttc 180
ttttatcccg cccccacccc caacctcagc ctcaagtatg taannnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnaaaac aaagccccgt tttgtcccca ggctggataa 300
caggggcgga atctgggtta attgaaccct ttgcttttgg ggttaaggca attttcctgc 360
ctcac 365

<210> 80
<211> 376
<212> DNA
<213> Homo sapiens

<400> 80
ggcacgagct ggaaaccagc ccctaagctg ctttcacctt cggcccattt ctcactagcc 60

agcctctccc acggcctccc cagtttcttc aaatacaccc cctccactat tcaccatact 120
gccaccgtga tttatttaca actttttgtc cggattacct cagtagcctt ctaattgtcc 180
cctttgcatc taaagtagcc cctctcatcc cccaaatctt accatgtcac tcttctacat 240
aattctggct ttccatgacc cataaaccac atttctcaag tgtgctctat gctggcttga 300
atatgttaat gatcttaatt ctacttttag tgcaattttc ttagagctgg catcactttc 360
atcatgacgt gagaac 376

<210> 81
<211> 384
<212> DNA
<213> Homo sapiens

<400> 81
ggcacgagag gattgtgtga aattgtgcaa atgcatgaat gtgggctggg atagtaaaag 60
ggagggcccc ggagcagccc acctggggtc ctatctagta gacgcgcccg gtgcccaccc 120
attgctgtga tgccagcagc ccactgcaag catcctcttc ctttccaagg ttctgtctgg 180
tacatgaata ggtgtggcag gggtgggggc tcctgaagac caactagggg tactagggac 240
cttagactct tgcgagagcc tgcaccccat atcaggtggg gtcaatagat aaataccccт 300
gcctccttgc cccttagttc tggtgtggtg ggcaagtcag aggaactgtt cttctcacac 360
tttcacgtgc tctcggtgga gatc 384

<210> 82
<211> 383
<212> DNA
<213> Homo sapiens

<400> 82
ggcacgagca aaggctcgca gcggccagaa acccggctcc gagcggcggc ggcccggctt 60
ccgctgcccg tgagctaagg acggtccgct ccctctagcc agctccgaat cctgatccag 120
gcgggggcca ggggcccctc gcctcccctc tgaggaccga agatgagctt cctcttcagc 180
agccgctctt ctaaaacatt caaaccaaag aagaatatcc ctgaaggatc tcatcagtat 240
gaactcttaa aacatgcaga agcaactcta ggaagtggga atctgagaca agctgttatg 300
ttgcctgagg gagaggatct caatgaatgg attgctgtga acaactgggg atttctttac 360
caggatcaca atggtaatat ggg 383

<210> 83
<211> 358
<212> DNA
<213> Homo sapiens

<400> 83
ggcacgagca gggccgcgcg gcggtgatca agcaccgctt ccccaagggc taccggcacc 60
cggcgctgga ggcgcggctt ggcagacggc ggacggtgca ggaggcccgg gcgctcctcc 120
gctgtcgccg cgctggaata tctgccccag ttgtcttttt tgtggactat gcttccaact 180
gcttatatat ggaagaaatt gaaggctcag tgactgttcg agattatatt cagtccacta 240
tggagactga aaaaaactcc ccagggtctc tccaacttag ccaagacaat tgggcaggtt 300
ttggctcgaa tgcacgatga agacctcatt catggtgatc tcaccacctc caacatgc 358

<210> 84
<211> 338
<212> DNA
<213> Homo sapiens

<400> 84
aagatggctg agagggacag aatgctttat tttggagaga aacaatgttc taggtcaaac 60
tgagtctacc aaatgcacac tttcacaatg ggtctagaag aaatctggac aagtcttttc 120
atgtggtttt tctacgcatt gattacatgt ttgctcacag atgaagtggc cattctgcct 180
gcccctcaga acctctctgt actctcaacc aacatgaagc atctcttgat gtggagccca 240
gtgatcgcgc ctggagagac agtgtactat tctgtcgaat accaggggga gtacgagagc 300
ctgtacacga gccacatctg gattcccagc agctggtg 338

<210> 85
<211> 475

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(475)
<223> n = A,T,C or G

<400> 85
gtcgctcaat aggcaggagt ccatcgattc gaattcggca cgagnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnc gctccactgt gcactcctga cacatacttt ccccgctaca ctctctattc 180
tccccctctt gtgttctctc tctatagcgg tagatagaga ggcctgtgtg tagataataa 240
acgtgtgtgt gtgtgtaaga aaggagacac aaacacgccc acnnnnnnnn nnnttggggc 300
ctttttttct tttgagccct ttggggaaaa aacccgggga aaacagccca tacccactat 360
ttggggcgcg ccaaaaaacc ttctttaaaa aaaatgtgtt aaatgttaaa ttttttagga 420
acannnnnnn nnnngcaaaa aatagcaccc caaaagcagg ggttttacat ttttg 475

<210> 86
<211> 467
<212> DNA
<213> Homo sapiens

<400> 86
gagcgatttt ctgcaggatt ctatcgattc gaattcggca cgagccatgg tctcagtgag 60
ggctggaatt tacagagaag tttggccagg gggtccacca tgctgccagt cagtttggga 120
aggaaacaga gaagctcggc catggggtcc accatggggt taatgaggcc tggaaggaag 180
cagagaagtt tggccagggt gtccaccatg ctgcctcgca ggtggggaag gaggaagaca 240
gagtggtcca aggcctccat catggcgtta gtcaggctgg aagggaggcg gggcagtttg 300
gccacgacat tcaccacaca gcagggcagg ctgggaaaga gggagacata gcagttcatg 360
gtgtccaacc tggggtccac gaggccggga aggaggcagg gcaatttggc cagggagttc 420
accataccct tgaacaggcc gggaaggaag caaacaaagc ggtccag 467

<210> 87
<211> 449
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = A,T,C or G

<400> 87
cggggtggga aaccngannt tnannaancg gacggattct cccgttccga atagcctttt 60
acagaagatt cttcacagct atgtgcctga agagatcang gatggaaatc aagttcgagt 120
tacctcatgg gatggcagga aatggggaga actggagggg gacacctatg accgggtgct 180
ggtggatgtg ccctgtacca cagaccgcca ctcccttcat gaggaggaga acaacatctt 240
taagcggtca aggaagaagg agcgacagat attgcctgtg ctgcaagtgc agcttcttgc 300
ggctggactc cttgccacca aaccaggagg ccatgttgtc tattctacct gctcactctc 360
acacttacag aacgagtatg tggtgcaagg tgccattgag ctcctgggca atcaatacag 420
catccaggta caggtggaag atctgactg 449

<210> 88
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 88
gtagtgtatg tgcagcctcc catcgattcg aattcggcac gagatcccct cttatatgat 60
gccccagccc aggagagata aaagcatcag caccatgaga ttcacctgcc tctggtcgtn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn actcttagac agcaaaaatg ctttctccca gtcttgttcc cttgttctca 300
gttcccaccc tgcctggata actactgttc ttggtttnnn nnnnnnnnnn nnnnnnnnnn 360
nagtctcgta ccagattcaa aaatcagtca actacttcaa aaacaatgac atgctggcta 420
cttagataga agaggaggc 439

<210> 89
<211> 436
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(436)
<223> n = A,T,C or G

<400> 89
ggcacgagca tcaaatagta aatatagatc ttatgctgga aatgtcaacc tccctggcag 60
ctgtaacgcc catcattgaa agggaaagcg gaggacacca ttatgttaat atgactttac 120
ctgtcgatgc agttatatct gttgctccag aagaaacatg gggaaaagtt cgtaaactcc 180
tggttgatgc aattcataat caactaactg acatggaaaa atgtattttg aaatatatga 240
aaggaacatc tattgtggtc cctgaaccac tgcacttttt attaccaggg aaaaaaaatc 300
ttgtaacaat ttcatatcct tcaggaatac cagatggcca gctgcaggcc tataggaagg 360
agttacatga tcttttcaat ctgcctcacg acagacccta tttcaaaagg tctaatgctt 420
atcactttcc agatgn 436

<210> 90
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(437)
<223> n = A,T,C or G

<400> 90
ggcacgagag atcatgcact accacatgca gcacgagcag taccggcagg tcatcagcgt 60
gtgtgagcgc catggggagc aggacccctc cttgtgggag caggccctca gctacttcgc 120
tcgcaaggag gaggactgca aggagtatgt ggcagctgtc ctcaagcata tcgagaacaa 180
gaacctcatg ccacctcttc tagtggtgca gaccctggcc cacaactcca cagccacact 240
ctccgtcatc agggactacc tggtccaaaa actacagaaa cagagccagc agattgcaca 300
ggatgagctg cgggtgcggc ggtaccgaga ggagaccacc cgtatccgcc aggagatcca 360
agagctcaag gccagtccta agattttcca aaagaccaag tgcagcatct gtaacagtgc 420
cttggagttg ccctcan 437

<210> 91
<211> 437
<212> DNA
<213> Homo sapiens

<400> 91
ggcacgagct tcagtcttat gtcatttact ctttaggaca acctcttgaa aaactaaatc 60
atttctttga aggtgttgaa gctcgcgtgg cacagggcat aagggaggag gaagtaagtt 120
accaacttgc atttaacaaa caagaacttc gtaaagtcat taaggagtac cctggaaagg 180
aagtaaaaaa aggtctagat aacctctaca agaaagttga taaacattta tgtgaagaag 240
agaacttact tcaggtggtg tggcactcca tgcaagatga atttatacgc cagtataagc 300
actttgaagg tttgatagct cgctgttatc ctggatctgg tgttacaatg gaattcacta 360
ttcaggacat tctggattat tgttccagca ttgcacagtc ccactaaacc ttgtgaaaga 420

agaaaagata actgaat 437

<210> 92
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(427)
<223> n = A,T,C or G

<400> 92
aacggctctt ctnctttga ggagcccatc gagtcgaatt cggcacgagg cgagtctctg 60
ggtcgcgacg ggaaggagtg aaacacctct ctgcgcctgc gcgctccgtg cctgcgaagc 120
aaacccggcc tcacctttc ctgcccgaag cagaagattc tcgcaggcct ggtttctccc 180
tccagaagac cccccaccca aatcctctgt agctcctggg agtgccctga cccctgctgc 240
caccgtcctt cagagagcaa cggaagagct tcccggaggg cgaggaaaag agggaaagta 300
gccagcaatg tcgaacgcag tgtataataa gatgtggcat cagacccaag aagccctcgg 360
tgctttactc gatgaagagc ctcagacgat gattgaacca cacagaaatc aggttttcat 420
ctttcaa 427

<210> 93
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(429)
<223> n = A,T,C or G

<400> 93
gtgacgatcc catcattcaa ttcggcacga gctcacagcc aaagttcctt ctgcccccag 60
gctgagagtg cttgatacac ccttgaatcc cctcttatat gatgccccag cccaggagag 120
ataaaagcat cagcaccatg agattcacct gcctctggtc gttagggaac aatggaggcc 180
tgcgatttgg agttaaactc tcagtgatct ctgtgttgac aacaccaaag ctagaggaat 240
ccagtaggat gtgggcatgg ttttcccgga aggctgactg agcagttctg caaatgtttg 300
caagtacagg gcagaatttc atccagcctc agaaccttga gccaagactc agcatcagca 360
aagccaaaag tttcatttct tcgactgtgg gagtgctagt cccaaccttt agatggccat 420
tcagttnta 429

<210> 94
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = A,T,C or G

<400> 94
ggcacgagat tatttacttg gtgtgtggtc accactgttt tttaaatgag tgttttcatt 60
tgtatcaaac tggacctgct ttcctcaagg attgcccaaa aggagacaca aatttactaa 120
acacttatca ataatagaac accgtgctag gcaatttcca tatactatta atttaatcct 180
cacaataact ttggaagaca gaaagtattt tctctgannn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn atcctctgtc tccaaagcct gtacttcatt caggacactt tcccccacat 360
ttagaaaagc tgtaattatc ttccagtgag acagcatagc acatgtgatc actgtccctt 420
c 421

<210> 95

<211> 421
<212> DNA
<213> Homo sapiens

<400> 95
ggcacgagat gagaagataa aattcagcgt tggcctttag actttgccat ccttaaggag 60
tgatggaagc caagtgaaca agcctcagtg acacaagtca aattcatagt ttcactctgg 120
gttttttgtt gttgtgtggt tattattctc actacagaaa gactgagttt catgctcctg 180
gctatgtcag atgtgaattt tcatgggtaa ctggacagtt aacaaaacag aagctgacaa 240
catagaagga cccatagcct tgaagttctc acacctttgc ctggaagatc ataacagtta 300
ctgcatcaac ggtgcttgtg cattccacca tgagctagag aaagccatct gcaggtgttt 360
tactggttat actggagaaa ggtgtctaaa attgaaatcg ccttacaatg tctgttctgg 420
a 421

<210> 96
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G

<400> 96
tggatccatc gattcaattc ggcacgaggt tatttttaag aacttttgct tactatattg 60
gatttacctg cggtgtgagt agctttaaat gtttgtgttt atacagataa gaaatgctat 120
ttctttctgg ttcctgcagc cattgaaaaa ccttttttcct tgcaaattat aatgtttttg 180
atagattttt atcaactgtg ggaaaccaaa cacaaagctg ataacctttc ttaaaaacga 240
cccagtcaca gtaaagaaga cacaagannn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnng 418

<210> 97
<211> 418
<212> DNA
<213> Homo sapiens

<400> 97
atgctacatt gctactttgt tgcattgatc gccagacgac cactagattc gaaactgagc 60
gcgagatgat gaatctgtgt gttatgaaaa tgcatgctac cagtataaaa tgacattctc 120
tattaataac atctgcggtg cgacacacat aattgtccca atttttaata ttgatgggga 180
gcatgaagca ttttttttaat gtgttggcag gccccattaa atgcataaac tgcataggac 240
tcatgtggtc tgaatgtatt ttagggcttt ctgggaattg tcttgacaga gaacctcagc 300
tggacaaagc agccttgatc tgagtgagct aactgacaca atgaaactgt caggcatgtt 360
tctgctcctc tctctggctc ttttctgctt tttaacaggt gtcttcagtc agggaggg 418

<210> 98
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(417)
<223> n = A,T,C or G

<400> 98
catcgattcg aattcggcac gaggccaagt ggacaggcca tagcccccac agactggagg 60
gacgcggcta gggaatgtcc cacagagtgg ccagttatcc ctgagagaaa gagcaggttt 120
tagcggagac tctgaggctg ctttagaata tggtgggtgt gtggggcaaa agggacaccc 180
aggggtgtat caagaggtca tnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnn 417

<210> 99
<211> 416
<212> DNA
<213> Homo sapiens

<400> 99
ggcacgagct acctcagccc tgctccagga gacaccagca gctgggccag tggccctgag 60
agatggcccc gaagggagca tgtggtgaca gtcagcaaga ggaggaacac atctgtggac 120
gagaactatg agtgggactc agaattccct ggggacatgg aattgctgga gactttgcac 180
ctgggcttgg ccagctcccg gctcagacct gaagctgagc cagagctagg tgtgaagact 240
ccagaggagg gctgcctcct gaacactgcc catgttactg gccctgaggc ccgctgtgct 300
gcccttcggg aggaattcct ggccttccgc cgccgccgag atgctactag ggctcggcta 360
ccagcctatc gacagccagt cccccacccc gaacaggcca ctctgctgtg aacatt 416

<210> 100
<211> 417
<212> DNA
<213> Homo sapiens

<400> 100
ggcacgaggg aaaatgtagg ctaccagtag aaaatgacat tctctattaa taagatctga 60
ggtgcgacac acataattgt cccaattttt aagattgatg gggagcatga agcatttttt 120
taatgtgttg gcaggcccca ttaaatgcat aaactgcata ggactcatgt ggtctgaatg 180
tattttaggg ctttctggga attgtcttga cagagaacct cagctggaca aagcagcctt 240
gatctgagtg agctaactga cacaatgaaa ctgtcaggca tgtttctgct cctctctctg 300
gctcttttct gctttttaac aggtgtcttc agtcaaggag gacaggttga ctgtggtgag 360
ttccaggaca ccaaggtcta ctgcactcgg gaatctaacc cacactgtgg ctctgat 417

<210> 101
<211> 412
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(412)
<223> n = A,T,C or G

<400> 101
ggcacgagga aagtaaacgt gtatctcttg ttcattttta tagaactttt gcatactata 60
ttggatttac ctgcggtgtg actagcttta aatgtttgtg tttatacaga taagaaatgc 120
tatttctttc tggttcctgc agccattgaa aaaccttttt ccttgcaaat tataatgttt 180
ttgatagatt tttatcaact gtgggaaacc aaacacaaag ctgataacct ttcttaaaaa 240
cgacccagtc acagtaaaga agacacaaga nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nn 412

<210> 102
<211> 414
<212> DNA
<213> Homo sapiens

<400> 102
ggcacgaggt cttgctcaca tgttgtacta ctctctcctg gatgtcactt gtcacctcta 60
ccagccctcc tttctccaga tggcttcttc ataaccacca ggtcagaaga ggatccgttc 120
caatgatttt cctaaaacaa tggaagtgtt ttccaaagag cttataaggc attgtaggat 180
ctggcctgcc ctgactccac tttaccagaa ccatctgctg ctcttctctc ttgtgttact 240
caaggtatta gctgctgtgg caaatcaact ctgaaatctc cgtgacttaa tacaagagag 300
gtttatttct tactcacgct gggtgcactg ccacttggta acagaggagc tatggaaact 360
tgagacctaa gcagaaatga gttcaataat attgctacac tctaggactt tctc 414

<210> 103
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(410)
<223> n = A,T,C or G

<400> 103
ggcacgagga agagccggga ggatgtattg gttgttagga aaatgtaggc taccagtaga 60
aaatgacatt ctctattaat aagatctgag gtgcgacaca cataattgtc ccaattttta 120
agattgatgg ggagcatgaa gcattttttt aatgtgttgg caggccccat taaatgcata 180
aactgcatag gactcatgtg gtctgaatgt attttagggc tttctgggaa ttgtcttgac 240
agagaacctc agctggacaa agcagccttg atctgagtga gctaactgac acaatgaaac 300
tgtcaggcat gtttctgctc ctctctctgg ctcttttctg ctttttaaca ggtgtcttca 360
gtcaaggagg acaggttgac tgtggtgagt tccaagacac ccaaggctan 410

<210> 104
<211> 411
<212> DNA
<213> Homo sapiens

<400> 104
ggcacgagat acgaatgggg tgtatttttc gactgctcgc aggcaccccc aggttatgtg 60
gacagagcta agcccaaagt tgtgattttc cactctgttc tgtccatgtc gagggaagat 120
aagtagaaag tgacacagta agagccagaa tacaccaggt gaaggagaga attgcattgt 180
gttttgagaa gtttcactga caagttatcc tgggctgtgg gacatcacta gctttgaaag 240
tgtagctggc acctcgtcca tctaatttga tgggtgtgtg tggggtgttg tgcacgcgtc 300
ggtctaacat atctgaaccc aggtgatttc tgttctcagg acgcttttag gtgacaagga 360
tcaggcatgt gaacaaataa ccatactgta aagctggctg tgctgggtct c 411

<210> 105
<211> 413
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

<400> 105
ggcacgagga agattctcgc agtcctggtt tctccctcca gaagaccccc cacccaaatg 60
ctctgtagct cctggtagtg ccctgacccc tgctgccacc gtccttcaga gagcaacgga 120
agagcttccc ggagggcgag gaaaagaggg aaagtagcca gcaatgtcga acgcaatgta 180
taataagatg tggcatcaga cccaagaagc cctcggtgct ttactcgata aagagcctca 240
gaagatgatt gaaccacaaa gaaatcaggt tttcatcttt caaacattag ccaccttcta 300
cgtaaagtat gtgcagatct ttagaaacct agagaatgtc tacgaccagt tcgtccaccc 360
ccagaaacga atactgatca ggaaagtcct ggacggngtg atgggccgca tcc 413

<210> 106
<211> 412
<212> DNA
<213> Homo sapiens

<400> 106
aggatcccat cgattctaat tcggcacgag ctccataagg cagaggtcta tgcgaggacg 60
cccggctgga ccacgagacc gcccattgat tgcgctggga caagaattcc ttatctttgg 120
aggcagtgaa acgactaata gctaaaggta atacagaaga actacgaaaa tgttttgggg 180
tccgaatgga gtttgtgaca gctggcctcc gagctgctat gggacctgga atttctcgta 240
tgaatgactt gaccatcatc cagactacac agggattttg cagatacctg gaaaaacaat 300

tcagtgactt atagcagaaa ggcatccgga tcagttatga cgcccgagct catccatcca 360
gagggggtag catcaaaagg tttgcccgac ttgctgcaac cacatttatc ag 412

<210> 107
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(408)
<223> n = A,T,C or G

<400> 107
ggcacgagga aaaaccagtt tctcttttat tgtctgttac taatctctat tctaaagatt 60
cagctcaatt ctcaaccata ctccaaactc tctcttttcc agctaccttt actccctctc 120
cttcaattcc actttcctct gcttacnnnn nnnnnnncnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnggnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn naatgttttt 360
tttcattaaa gagagaaatc acctattcag gaccggcccc cacctttg 408

<210> 108
<211> 405
<212> DNA
<213> Homo sapiens

<400> 108
ggcacgaggc ttacaggggt gaccagggcc cttcctaact cgaccgcatg tggattggtg 60
gctggcttgg gagggaggct gtccgatgct gacattcccc ttaacatggc cctgaccgtg 120
gctgtcaggg gccaccttgc ctcaccaggc cagcccccact gggaatgggg tcagtcacag 180
cagaaccgtc caaaggtgga cctgatgtgg gccctgccgg gggcgcttgg cctcagcggg 240
ccatgggaga cccagtgaaa cgactctagt gtgaggcagt ggtcctgcca ctgactgaca 300
aaccctcttt gtaagcaaac ttgacaaata atgaatctac tgaactctgt tatagaacaa 360
gctcattctg catgaacttc tcttattgaa gcagaagcca cgtca 405

<210> 109
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

<400> 109
ggatcccatc gnttcgnatt cggcacgagg caaccagctc gtccagcgcg tggccctgct 60
gctcaaggag cagactgcgt accccccgac acactacatc cggagggtgc cccagaggaa 120
gatccactac ttcacgggcc tgcaggcgct tcagctgctg ctgctgtgtg ccttcggcat 180
gagctccctg ccctacatga agatgatctt tcccctcatc atgatcgcca tgatccccat 240
ccgctatatc ctgctgcccc gaatcattga agccaagtac ttggatgtca tggacgctga 300
gcacaggcct tgactggcag accctgccca cgccccattc gccagccctc cacgtactcc 360
caagctggct ctggaactgt gaggggaagg ggaagatgtg tgg 403

<210> 110
<211> 397
<212> DNA
<213> Homo sapiens

<400> 110
ggcacgagtc tgcttctgtc actgtcacat agacagccct gcatgccccc tgtctcacac 60
aggttgtaat gaagacagct ccttctcatc tttccataag cctgagatac aagttcaggg 120

actcagcaat gcactttagg actgagctag gaggcaaata tctgaagctt gctatgctgt 180
tctttccatt ccttttccct ctgaaacaca caaaatacca aaggaactta cgcaacacac 240
cactgagtcc tctaactaat catatgtgct cagacacagc tcaagcacac cccttagtta 300
agaaagaacc tccatataca ttaatttttt tctgcctaaa aataaaattg cgttgtggca 360
gcaatttgga aactacagca aagtctccaa aaaaatc 397

<210> 111
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 111
ggcacgagag ccgttgcctt caccgccctt tctcctttta tccttttttta aacgctcttg 60
ggggttatgt ccgctgcttc ttgggtgccg agacatatag atggtggtct cgggccagcc 120
cctcctctcc ccgccttctg ggaggaggag gtcacacgct gatgggcact ggagaggcca 180
gaagagactc acaggagcgg gctgccttcc gcctggggct ccctgtgacc tctcagtccc 240
ctggcccggc cagccaccgt ccccagcacc caagcatgca attgcctgtc ccccccggcc 300
agcctcccca acttgatgtt tgcgttttgt ttggggggat atttttcata attatttnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn c 401

<210> 112
<211> 401
<212> DNA
<213> Homo sapiens

<400> 112
ggcacgaggg cagtccagca acaagccttt catttacatt aaattataac ttttcattca 60
ttcctaaacc aaacttaaaa ttctgctttc ctttgagtag aaggtattta acttgttttg 120
tttttccttc agaaggaatt taatgcaaac ggattgcagt cagcactttc tgaatgtttt 180
cacacagtat gcaaagctta catcatacca aggagtggag agttgaagtt tcctcccagt 240
gactccagtg acagaccaca cctagaaagc gtttctcttc ctgagtattt caaaaagatg 300
taaaagagct ggggagagta tgggaagaaa caatacagga ttgcctttaa ttaattaaga 360
attgcctcct gataaaagga aaaagaaatt aatgctggag g 401

<210> 113
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 113
ggcacgaggc cccacgggcc ccatctcccc acaggcattg agggtaactg gggtaggctc 60
ctggagcagg tgggcaccat ggctttgtgg gccagccaaa gggaaaagga ggtgcttagg 120
agggaaaggg cagtggaatg gcgggagagg gctgtggaaa aaagggagcg agccctggag 180
gaggtggaaa gggccatcct ggagatgaag tggaaggtga gggctgagaa ggaggcatgc 240
cagcgggaga aagagctgcc tgcagcagta catcccttcc attttgttta aattgggctt 300
ggagaatcta ttctgaaaac attgactcta gacttgtaga anagagccat tttaattttc 360
accttcaatg gtaaaagcaa gggtaatttg gttgacattt t 401

<210> 114
<211> 399
<212> DNA
<213> Homo sapiens

<400> 114
ggcacgagag cagaagattc tctcagtcct ggtttctccc tccagaagac cccccaccca 60
aatcctctgt agctcctggt agtgccctga cccctgctgc caccgtcctt cagagagcaa 120
cggaagagct tcccggaggg cgaggaaaag agggaaagta gccagcaatg tcgaacgcaa 180
tgtataataa gatgtggcat cagacccaag aagccctcgg tgctttactc gataaagagc 240
ctcagaagat gattgaacca caaagaaatc aggttttcat ctttcaaaca ttagccacct 300
tctacgtaaa gtatgtgcag atctttagaa acctagagaa tggctacgac caggtcgtcc 360
acccccagaa acgaatactg atcaggaaag tcctggacg 399

<210> 115
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(399)
<223> n = A,T,C or G

<400> 115
ggcacgaggc tttttccaac ttttaaggat atcaggagag aagacactct tgatgtggag 60
gtttctgcca gtggctacac aaaggaaatg caggcagatg atgaactgct tcatccatta 120
ggtccagatg ataaaaatat tgaaacaaaa gagggatctg aattctcatt ttcagatgga 180
gaagtggcag aaaaagcaga ggtttacagg tcagaaaatg aaagtgaacg gaactgtcta 240
gaagaatcag agggctgcta ttgcagatca tctggagacc ctgaacaaat aaaggaagac 300
agtttatcag aagagagtgc tgatgcacgg agttttgaaa tgactgaatt caatcaagct 360
ttataagaaa taaaagggca ggttgttgaa aacaactcn 399

<210> 116
<211> 400
<212> DNA
<213> Homo sapiens

<400> 116
ggcacgagcg gaccgggccg agccgggccg cccgggcgca gtctttaacc atggcgtccc 60
tcttcaagaa gaaaactgtg gatgatgtaa taaaggaaca gaatcgagag ttacgaggta 120
cacagagggc tataatcaga gatcgagcag ctttagagaa acaagaaaaa cagctggaat 180
tagaaattaa gaaaatggcc aagattggta ataaggaagc ttgcaaagtt ttagccaaac 240
aacttgtgca tctacggaaa cagaagacga gaacttttgc tgtaagttca aaagttactt 300
ctatgtctac acaaacaaaa gtgatgaatt cccaaatgaa gatggctgga gcaatgtcta 360
ccacagcaaa aacaatgcag gcagttaaca agaagatggg 400

<210> 117
<211> 402
<212> DNA
<213> Homo sapiens

<400> 117
ggcacgaggg gagatcgctc agctggccgt gtcctggcag gccacggcat atgcctccaa 60
ggacggggtc ctcactgagg ccatgatgga cgcctgtgtg caagatgctg tccagcagta 120
ccgacagaag atgcgctggc tgaaggcgga ggggcctggg cgcggggtcg agcacccccct 180
atccggagtc caaggcgaga ccctcacctc atggagcctg gccacggacc cctcctaccc 240
ctgccttgcc ggcccctgca catttaggat atgctcctgg atggggactg ggctgtgccc 300
agggcctctg tcccccagga tgtcttgtgg tggcggtcgg ccgttctgcc ccccagggca 360
ccccctgttg taggcactgg ctctaggagg gcaggcctcc tt 402

<210> 118
<211> 395
<212> DNA
<213> Homo sapiens

<400> 118
ggcacgaggt agagatacga atggggtgta gtagccgact gctcgcaggc acccccaggt 60

tatgtggaca gagctaagcc caaagttgtg attttccact ctgttctgtc catgtcgagg 120
gaagataagt agaaagtgac acagtaagag ccagaataca ccaggtgaag gagagaattg 180
cattgtgttt tgagaagttt cactgacaag ttatcctggg ctgtgggaca tcactagctt 240
tgaaagtgta gctggcacct cgtccatcta atttgatggg tgtgtgtggg gtgttgggca 300
cgcgtcggcc tagcagatct gaacccaggt gatttctgtt ctcaggaagc ttttaggtga 360
caaggatcag gcatgtgaac aaataaccat actgg 395

<210> 119
<211> 144
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(144)
<223> n = A,T,C or G

<400> 119
ccggtaagga atatacttct tctgatacta aatatgccaa tatttaaaat gtaatattca 60
gggattacaa ctgtgagggc taaacacacg gaattaccca ccaattcctc tgtagttctc 120
tactaattca attttgcatc ctcn 144

<210> 120
<211> 392
<212> DNA
<213> Homo sapiens

<400> 120
ggcacgagac caggtcataa gaggatccgt tccaatgatt ttcctaaaac aatggaagtg 60
ttttccaaag agcttataag gcattgtagg atctggcctg ccctgactcc actttaccag 120
aaccatctgc tgctcttctc tcttgtgtta ctcaaggtat tagctgctgt ggcaaatcaa 180
ctctgaaatc tccgtgactt aatacaagag aggtttattt cttactcacg ctgggtgcac 240
tgccacttgg taacagagga gctatggaaa cttgagacct aagcagaaat gagttcaata 300
atattgctac actctaggac tttctccaaa attaacaaca gaacaaaagt gcaaggcagt 360
gataacccat ctgacagcat ttggggagtg tt 392

<210> 121
<211> 395
<212> DNA
<213> Homo sapiens

<400> 121
ggcacgagat caatcacaaa agtttatcct taagacttcc cttcagctgc tggaaggcag 60
tcatcacatc tgtgaaaaga gtgctagtta taacaaatga gatcacaaat ttgaccattt 120
tattagacac cctctattag tgttaacaga caaagatgaa ggttaagttg aaatcaaatt 180
gaaatcatct tccctctgta cagattgcaa tatctgataa taccctcaac tttcttggtg 240
caaattaatt gcctggtact cacagtccag tgttaacagg caataatggt gtgattccag 300
aggagaggac taggtggcag gaaaataaat gagattagca gtatttgatt ggagccataa 360
gcataatttg gttccggcgg cggccaggtt taaaa 395

<210> 122
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(288)
<223> n = A,T,C or G

<400> 122
cgcccgcgcc tctctgttct ctctcgcgcg cggtgtctct ctcgatagag tgcgcgacct 60
gcacaccctc tgtgtggggt tctcgctccc cgtgtgcgcg cgcgcgcgct ctctgtggga 120

ctcgcacaca ccgcgcgcgc gcgcgctctc tgtggggggg ccctccccgc accttgtgtg 180
tgtgtgtctg tgttatctct gtgagatgtg cgtgnnnnnn nnnnntctgt gtgtgtgtct 240
gccctccgcg ccgtgtctgt tatatatgcg ctcgctcgct ggggcgcg 288

<210> 123
<211> 393
<212> DNA
<213> Homo sapiens

<400> 123
ggcacgagga tccattcttc gacccccaga tgtgactcta aagaaggctg aaaatttttg 60
tccaaattgc catgcagata tcttgaacag caggacattt gcaggccttg tctactggac 120
ttttctccca aacaggacaa gcccaggcag ggctgcatgg agaggaatgg aacctggagc 180
tagaattaat tgcccactct cccaccctac cagtgcagcc cggcaagggc aggaattggg 240
aggcctaagg tgggcatgaa agcttgggaa gcactgtcgt ctctcagaca ggcgtcctaa 300
agacctctag gctggaagct tgggcttgca agtggatccg ggaccgaggg tggtctcttg 360
gacaacccca ggaacttgga ccaaggcaga gcc 393

<210> 124
<211> 394
<212> DNA
<213> Homo sapiens

<400> 124
ccgcgacgag atgatgatct gcttcttcca ttatgcccag atgataaaaa ggattgatac 60
aaaagaggga tctgaattct cattttcaga tggagaagtg gccgaaaaag cagaggttta 120
caggtcagaa aatgaaagtg aacggaactg cctagaagaa tcagagggct gctattgcag 180
atcatctgga gaccctgaac aaataaagga cgacagttta tcagaagaga gtgctgatgc 240
acggagtttt gaaatgactg aactcaatca agctttagaa gaaataaaag ggcaggctgt 300
tgaaaacacc tctgtaactg aattttctga ggagaaacac cgaacttgaa attcacaccg 360
gcctaatgtc caagaattca aggggggtc cctc 394

<210> 125
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(390)
<223> n = A,T,C or G

<400> 125
ggcacgagcc cttatacaaa catatatgaa catatatact ttttttgttg tataaaaaca 60
ggatcacatt atagatatta ttctgtaact ttctgttttc acccaaaata cagcagagca 120
ctattttcca gaagcacgta gttctaactt nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnaactt tattcaagta cttcacattt taagtggaca ttccatttgt 240
ctgctataat ttacaattat agcaatactt tgagaaaggt ctttgcaagt atatccatat 300
gaactaatgt ctatgtagaa gatatgctgg ctcaaatatt atgtacattt aatgtcttaa 360
taaacaccgc tagattactt tccaggaagc 390

<210> 126
<211> 388
<212> DNA
<213> Homo sapiens

<400> 126
ggcacgaggt cagcacacat tactttaaca ctttggactt gaaattctga aagatcagaa 60
attccttact gtttgagatg attaggtttt agggactagc cattttatct cacatgactc 120
aggccttaat gctccattgc taatagctaa atgtggaaaa gtttagaatt acatttaatt 180
tagtcaactg ttaggctgca atcatttttt tttaaaaatc tgcttatggc attattcgag 240
ataacttgac caactctaaa atatatatgt aattacttct agatgtaagt agtttttcat 300
attaacaaca caatcaggct ctgtttcagt tagttcttag agtggtgaaa aaaaatcttt 360

acagtaagtg caaaattata atccaagg 388

<210> 127
<211> 388
<212> DNA
<213> Homo sapiens

<400> 127
ggcacgagag ttaatccaaa agacttccct tcagctgctg gaaatcagtc atcacatctg 60
tgaaaagagt gctagttata acaaatgaga tcacaaattt gaccatttta ttagacaccc 120
tctattagtg ttaacagaca aagatgaagg ttaagttgaa atcaaattga aatcatcttc 180
cctctgtaca gattgcaata tctgataata ccctcaactt tcttggtgca aattaattgc 240
ctggtactca cagtccagtg ttaacaggca ataatggtgt gattccagag gagaggacta 300
ggtggcagga aaataaatga gattagcagt atttgacttg gagccatagg catcaattct 360
gctccagctg tcgaccaggt tctaaaaa 388

<210> 128
<211> 267
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(267)
<223> n = A,T,C or G

<400> 128
actgtgtgtg tgtctgtttt ctctctctct cttctcagtc acactttttt tttgggacac 60
accctccatc cgcggggggg tttttttccc ggcgcgcgcc cttttttttt gtgtgtttct 120
ctgcgcgcct ctcttttttc tctctcttcc cccccgctt annnnnnnnn nnnnnngcgg 180
gggggtttt cgcgcgttcn nnnnnnnnnn nnctcttccg ccccccaca gggggtgct 240
gtttattatc tttctttctc cctgagc 267

<210> 129
<211> 389
<212> DNA
<213> Homo sapiens

<400> 129
ggcacgagct tgactgcaaa cttgctgaag gtagggactg tttgtcttgg acttcgctgc 60
cagtccttag aacagtgtct gggacacagt gtgttctcaa atatttgttg ctggaataaa 120
tgaatgaact aaatcagtct tttagggatt tactgttaac caccatggga aaattaaata 180
aatgcgggga aggaaaacgt tctaaaatta gaagactact ttctactctc agcttctgat 240
tccctctgag ctaagaacca gacagcctta ggctggtaac tcctataagc tggtcctcct 300
cccatgctga ccccatcttt actgtacaat tcacttttca tggactgaag gcaccaccaa 360
gatagatcca ggagtgacaa ctccagtgg 389

<210> 130
<211> 319
<212> DNA
<213> Homo sapiens

<400> 130
tgttgtaact gggagtggag gcccagtggc tggggagaca ttaggtggtg gggcccagcc 60
cgacctccag gttcttcctt ctccctagct gttgctttgg tctggccact cccagccccc 120
ttgtcccctt ggaagcttgc cctgccctca tcttgcccat gccttctact gccaggagac 180
ttgcacccat ttcaacccta gggcgggggc aagtggggca aggatggacc agcagaaggg 240
gggtaaggct ctgttcactt ccccctgcct ccacagaacg aagccacgga ttccgttatc 300
ttcctccagt tttgttcct 319

<210> 131
<211> 385
<212> DNA

<213> Homo sapiens

<400> 131
ggcacgagaa acgtttcagc tacgaaagtg agctttttcc aacttttaag gatatcagga 60
gagaagacac tcttgatgtg gaggtttctg ccagtggcta cacaaaggaa atgcaggcag 120
atgatgaact gcttcatcca ttaggtccag atgataaaaa tattgaaaca aaagagggat 180
ctgaattctc attttcagat ggagaagtgg cagaaaaagc agaggtttac aggtcagaaa 240
atgaaagtga acggaactgt ctagaagaat cagagggctg ctattgcaga tcatctggag 300
accctgaaca aataaaggaa gacagtttat cagaagagag tgctgatgca cggagttttg 360
aaatgactga attcaatcaa gcttt 385

<210> 132
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 132
ggcacgaggg gaatagaggg tccctggtga cagggcaagg ctagatctgg agcctgcact 60
tggcctgtga catactgtct tgtttctgag aatcctcccc tacttctcta gataatctcc 120
aaacacttct gtgactactt aatcacaaag gaaattttca ggagatataa tcgaattcta 180
ttttacaaaa aaaaagagaa gggatctgaa tgttttcagt tcacgctagg gatcnnnnnn 240
nnnnnnnnnc ccaaacctga cgtttgagga cccgcctttt tttcagccaa tttaaaagat 300
tttttaaggt ttagggttgg ttggccatta aaccatcccc ggaaagaaaa tggggggtaaa 360
agaccaagaa ggaggtcgcc aag 383

<210> 133
<211> 382
<212> DNA
<213> Homo sapiens

<400> 133
ggcacgagat aagatctgag gtgttacaca cataattgtc ccaattttta agattgatgg 60
ggagcatgaa gcattttttt aatgtgttgg caggccccat taaatgcata aactgcatag 120
gactcatgtg gtctgaatgt attttagggc tttctgggaa ttgtcttgac agagaacctc 180
agctggacaa agcagccttg atctgagtga gctaactgac acaatgaaac tgtcaggcat 240
gtttctgctc ctctctctgg ctcttttctg ctttttaaca ggtgtcttca gtcagggagg 300
acaggttgac tgtggtgagt tccaggacac caaggtctac tgcactcggg aatctaaccc 360
acactggggc cttgaatggc ca 382

<210> 134
<211> 375
<212> DNA
<213> Homo sapiens

<400> 134
ggcacgagca agcctttcat ttacattaaa ttataacttt tcattcattc ctaaaccaaa 60
cttaaaattc tgctttcctt tgagtagaag gtatttaact tgttttgttt ttccttcaga 120
aggaatttaa tgcaaacgga ttgcagtcag cactttctga atgttttcac acagtatgca 180
aagcttacat catacaagg agtggagagt tgaagtttcc tcccagtgac tccagtgaca 240
gaccacacct agaaagcgtt tctcttcctg agtatttcaa aaagatgtaa aagagctggg 300
gagagtatgg gaagaaacaa tacaggattg cctttaatta attaagaatt gcctcctgat 360
aaaaggaaaa agaaa 375

<210> 135
<211> 376
<212> DNA
<213> Homo sapiens

<400> 135
ggcacgagac ctgtttgagg tggaactcca agcagctcgc accttggagc gactggagct 60
ccagagtctg gaggcagctg agatagagcc ggaggcccag gcccagaggt cgcccaggcc 120
cacgggctca gatctgctcc ctggagcccc catcctcagt ctgcgcttct cctacatctg 180
ccctgaccgg cagttgcgtc gctatttggt gctggagcct gatgcccacg cagctgtcca 240
ggagctgctt gccgtgttga ccccagtcac caatgtggct gttcccctgc aggatctgag 300
tggcatagag ctgggcctgg caggccagag cctgcggcta gagtgggcag ctggggcggg 360
ccgctgtgtg ctgctg 376

<210> 136
<211> 371
<212> DNA
<213> Homo sapiens

<400> 136
ggcacgaggt cacctctacc agccctcctt tctccagatg gcttcttcat aaccaccagg 60
tcagaagagg atccgttcca atgattttcc taaaacaatg gaagtgtttt ccaaagagct 120
tataaggcat tgtaggatct ggcctgccct gactccactt taccagaacc atctgctgct 180
cttctctctt gtgttactca aggtattagc tgctgtggca aatcaactct gaaatctccg 240
tgacttaata caagagaggt ttatttctta ctcacgctgg gtgcactgcc acttggtaac 300
agaggagcta tggaaacttg agacctaagc agaaatgagt tcaataatat tgctacactc 360
taggactttc t 371

<210> 137
<211> 258
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(258)
<223> n = A,T,C or G

<400> 137
cagtttcttt gtgcgcgcgc cccccctttt ttctctctct ctccgcgcgg gcgtgtccct 60
ccnnnnnnnn nnctgtgtgt gcgctctctc cgccccatat atattgtgtt tttctctgtg 120
gannnnnnnn nntctctcta gagtcttttc tctcccctcg cgcgcacatt gttatacact 180
cctcccctct ctttcttttt acacacacat atatattgcg cccctctccc cccacacatt 240
tatatctctc tcacatct 258

<210> 138
<211> 368
<212> DNA
<213> Homo sapiens

<400> 138
ggcacgagac attttgagac ttcttccaaa ttggtcccta gaaagttaca ctggtttgta 60
ctctcactta tgtcactgtt tataccacca ctgactgctg cctgctttat tatttcttta 120
atgagttgga ctgaacagtg gttaatcctg actctgtttt tgactgacag ttaacagtta 180
catgaaccat tcatattaca gctcttactt aaatttgacc aagccaggat atatctgtta 240
ggccacattc atttagggat catgttttcc aaagcaggtt tgggcaaaat taatccacag 300
gactgaaagg tatacatctg tgagttttgt tctcacttcc acctctaatt tgaagaacac 360
tttaattg 368

<210> 139
<211> 372
<212> DNA
<213> Homo sapiens

<400> 139
acggcacgag ctggctcctc gttttctttg tggacagtct cattaccaac atcctcgttc 60
gggtctagga tgcctttctg ctcgagggga ccaacgcggc gattcgctat gccttggcca 120
ttatcttgta caacgagaag gacatcttga ggctacagaa tggcctggaa atctaccagg 180

acctgcgctt cttcaccaat accaactcca tcagccggaa gctgatgaac attgccttca 240
atgacatgaa ccccttccgc atgaaactat tgcggcagct gtgcatggcc caccgtgagc 300
ggctggaggc tgatctgccg gagctggagc aacttaaggc aaagtacctg gctaggcagg 360
catcccggcg ca 372

<210> 140
<211> 365
<212> DNA
<213> Homo sapiens

<400> 140
ggcacgaggc tgagagtgct tgatacaccc ttgaatcccc tcttatatga tgccccagcc 60
caggagagat aaaagcatca gcaccatgag attcacctgc ctctggtcgt tagggaacaa 120
tggaggcctg cgatttggag ttaaactctc agtgatctct gtgttgacaa caccaaagct 180
agaggaatcc agtaggatgt gggcatggtt ttcccggaag gctgactgag cagttctgca 240
aatgtttgca agtacagggc agaatttcat ccagcctcag aaccttgagc caagactcag 300
catcagcaaa gccaaaagtt tcatttcttt gactgtggga gtgctagtcc caacctttag 360
atggc 365

<210> 141
<211> 353
<212> DNA
<213> Homo sapiens

<400> 141
ggcacgagaa acaaaagaga gcaagagaga agacagtggg tgaagtcctg gttccagact 60
cccctttttg ccgggatatg atggatctgt cagctggtga ggcccctcta agaggggtgg 120
tatcttcggg ccaggtgcct agagtcctag agagctagag atggagggaa attcagatca 180
tctaaaccct tcagcccttc actggacaga agaggaaact gaggctccat ctgcatgacg 240
ttcccagagt cacggcacaa attcatggaa gaagcagcag gaaactcagt tctccagtct 300
gggtccaatg tgtgttttag aaatatctcc acagggttaa tgactcaatt ttt 353

<210> 142
<211> 352
<212> DNA
<213> Homo sapiens

<400> 142
ggcacgaggc cactcggggg cccaggaacc cctcagttag ggcttctcag tcactgagcg 60
gaaggtgccc ccagaggggg cagccgcctg tgaggagcag gcgtgtctgg gtaaccatgt 120
ggctcctgct ggcctcccct gcctgtcccc aaagcacagg gctcagctcc agagggagac 180
gggctgggct gtcagtggtc ccaggtgcat cccactttcc agcagcactt ggtgccagca 240
gaggctgcag gtgtggcagg aggggcccca gccgtgaggg caccaggttc aggcccggca 300
tctcagggtg gagagccagg gctgtcctga acctccagag ggggtgagct gg 352

<210> 143
<211> 470
<212> DNA
<213> Homo sapiens

<400> 143
gacttctgtc tttttaggat cccatcgact tcaattcggc acgaggtcat gagaaaggaa 60
ccaatggagt atgagaagtt tccagtgaaa aacagaaaga atccagtaga atttatttag 120
ggaagaggaa aagatgtgtt cggggtggcc ttggaagtga acgttgaagg actactgaga 180
ttggttcaag aaactgtgaa gggaaagaaa gggttatact gagaaatgga agagataatt 240
ttagaaactt gcgaaaaatg gcttaatcta aatgagtgtt aggggagata cagctgtgat 300
gataggttga gctcacatgg tggagagcca cagttgcggg tgcttgcact gataatgtga 360
gggcatggag acagacaata agttgaatgc tcttttttta acaaaggaag ctaaaaggga 420
gggggatgct aatttgatca atacgtttgg gaaaacttat attttcttgg 470

<210> 144
<211> 456
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(456)
<223> n = A,T,C or G

<400> 144
tagcactttt gtttaggagg accccatcga ttcgaattcg gcacgagctg cactgagcag 60
caccggtgtt cttcatccgg ctgcaccccc aacagagctc tttcttcccc agatcccttt 120
tacagttgga ttctccctct tggatctggc tctgccttag tccgacctag agggatcagc 180
ttcgcccacg cccactctca cccggaacct ttcatctctt attgaagcct tttaggccca 240
ttgggatgtt cattagaact ctgaaaacta cagttctccc ctttatgagg actgcaccac 300
agctcgccct ctcctgggtt ccgcctggtt gcagagtgag cccatgggac agccctctga 360
aattatactg cttacaacca tgctgagtct gcaaggactt cgtccaagcc tttccgtcca 420
ggacctcaaa cagatccaat cacaagaaga gagatn 456

<210> 145
<211> 464
<212> DNA
<213> Homo sapiens

<400> 145
atcgcccata cggcgagccc accgacgcga attcggcacg aggggaaaca caggcctctt 60
ctgcttttag gaccctcccc ctgccttgca gggggctcgg ggagagcaat atcaggagct 120
agggcttgct gctgcccaca ctcctgcttt ttgggatatc taactgctaa ggagggagtt 180
gacatccccc ttctggctca tgtgtctgac accaacaaca tgggctctgt ccctctctct 240
ttgactctcc ctttgtcctc cccatacagc tggggtgggg tggatcccta tacctggggc 300
aggcagcccc aaagtggtgg agggggatgg caaagactgt ataggcgcca ctggactctg 360
gcaaggcctt tattaccttt actccccttc ctctcccatc accagcctca aggcctgagg 420
tgtgcagggg ctcctggcag ctactgagtg agggttcctg gtcg 464

<210> 146
<211> 448
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(448)
<223> n = A,T,C or G

<400> 146
ggcacgagct gcactgagca gcaccggtgt tcttcatccg gctgcacccc caacagagct 60
ctttcttccc cagatccctt ttacagttgg attctccctc ttggatctgg ctctgcctta 120
gtccgaccta gagggatcag cttcgcccac gcccactctc acccggaacc tttcatctct 180
tattgaagcc ttttaggccc attgggatgt tcattagaac tctgaaaact acagttctcc 240
cctttatgag gactgcacca cagctcgccc tctcctgggt tccgcctggt tgcagagtga 300
gcccatggga cagccctctg aaattatact gcttacaacc atgctgagtc tgcaaggact 360
tcgtccaagc ctttccgtcc aggacctcaa acagatccaa tcacaagaag agagatttca 420
ggaaagagaa nattattcct atcatcgn 448

<210> 147
<211> 439
<212> DNA
<213> Homo sapiens

<400> 147
ggcacgagga aagttaagca actacaggaa atggctttgg gagttccaat atcagtctat 60
cttttattca acgcaatgac agcactgacc gaagaggcag ccgtgactgt aacacctcca 120
atcacagccc agcaagctga caacatagaa ggacccatag ccttgaagtt ctcacacctt 180
tgcctggaag atcataacag ttactgcatc aacggtgctt gtgcattcca ccatgagcta 240
gagaaagcca tctgcaggtg ttttactggt tatactggag aaaggtgtga gcacttgact 300

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ttaacttcat atgctgtgga ttcttatgaa aaatacattg caattgggat tggtgttgga      360
ttactattaa gtggttttct tgttattttt tactgctata taagaaagag gtgtctaaaa      420
ttgaaatcgc cttacaatg                                                    439

<210> 148
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 148
ccccgcgcgc gctccctctc tatcttttat acaaaatata gagagcgcac atctctgtgt       60
gtgagagagt ctgtgcgcgc gcgcatatat atatgggagg ggtgtctccc cccatctgtg      120
tgtctctcct cttgcggggc atatgcgtgc gcacacccgc gcgctgtgtc tcttttgtgc      180
cnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn      240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnncg cgcgcacaca cccacacacc      300
gtgtgttcta cagcgcgata aagagagaca caca                                   334

<210> 149
<211> 428
<212> DNA
<213> Homo sapiens

<400> 149
ggcacgaggt cctgagcagc ctcatgggag gtgaattaga gaaaacaaaa gagagcaaga       60
gagaagacag tgggtgaagt cctggttcca gactcccctt tttgccggga tatgatggat      120
ctgtcagctg gtgcctagag tcctagagag ctagagatgg agggaaattc agatcatcta      180
aacccttcag cccttcactg gacagaagag gaaactgagg ctccatctgc atgacgttcc      240
cagagtcacg gcacaaattc atggaagaag cagcaggaaa ctcagttctc cagtctgggt      300
ccaatgtgtg ttttagaaat atctccacag ggttaatgac tcaatttttc atgcatgatt      360
gctagtaatg acaatcatgt tatgtttggt tctgtagctt tggaaatcac tccttccact      420
tgagtttc                                                                428

<210> 150
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(427)
<223> n = A,T,C or G

<400> 150
cgccccaaan nnnaatctct aaaggggtaa gggagatacc taccttgtct ggtaggggag       60
atgtttcgtt ttcatgcttt accagaaaat ccacttccct gccgacctta gtttcaaagc      120
ttattcttaa ttagagacaa gaaacctgtt tcaacttgaa gacaccgtat gaggtgaatg      180
gacagccagc caccacaatg aaagaaatca aaccaggaat aacctatgct gaacccacgc      240
ctcaatcgtc cccaagtgtt tcctgacacg catctttgct tacagtgcat cacaactgaa      300
gaatggggtt caacttgacg cttgcaaaat taccaaataa cgagctgcac ggccaagaga      360
gtcacaattc aggcaacagg agcgacgggc caggaaagaa caccaccctt cacaatgaat      420
ttgacac                                                                 427

<210> 151
<211> 437
<212> DNA
<213> Homo sapiens

<220>
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<221> misc_feature
<222> (1)...(437)
<223> n = A,T,C or G

<400> 151
ccgagccgga tgnccttnnn gagtatngca angattccaa ttcggcacga gagacagtgg 60
catggagctt tgaaagacga gtaggtgtta gcaaggaaat aaggaggaac gggggttacg 120
ggcagaggag aaagcacatg ccaagtcagc aaagaaaagt agaattcgaa aactttttaa 180
aaatattact aaggattttc acaatgctgc actgggctag aaactgaagc taaaacagat 240
acgtggtccc tgctgctatg gggcttacgt tctacaggca aggacaggtt gtgatgaggg 300
ttctgaagga tagagaccaa gcatggaggg tgttgaggag gcttctgcga gacctgaatg 360
atgggaagcc acgaagtggg aggggtgggg gtccaggctg gaggggccca atgtatgtgt 420
agagggacta cagccct 437

<210> 152
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

<400> 152
ggcacgagct gcactgagca gcaccggtgt tcttcatccg gctgcacccc caacagagct 60
ctttcttccc cagatccctt ttacagttgg attctccctc ttggatctgg ctctgcctta 120
gtccgaccta gagggatcag cttcgcccac gcccactctc acccggaacc tttcatctct 180
tattgaagcc ttttaggccc attgggatgt tcattagaac tctgaaaact acagttctcc 240
cctttatgag gactgcacca cagctcgccc tctcctgggt tccgcctggt tgcagagtga 300
gcccatggga cagccctctg aaattatact gcttacaacc atgctgagtc tgcaaggact 360
tcgtccaagc ctttccgtcc agggacctca acagatccaa tcacaagaag agagatttca 420
ggaan 425

<210> 153
<211> 421
<212> DNA
<213> Homo sapiens

<400> 153
ggcacgagcc gtggctgcct cgtgagcctc ccagagccca ggcctccgtg gcctcctcct 60
gtgtgagtcc caccaggagc cacgtgcccg gccttgccct caaggatttt tgcttttctc 120
ctgtgcacct ggcgaggctg aaggcgaggg gtggaggagg ccccagcaca gcctcatctc 180
catgtgtaca cgtgtgtacg tgtgtatgcg tgtgtgtacg tgtgtatgcg tgtgtgtacg 240
cgtgtgtacg tgcgtgtgta cacatgcgtg gccgcctgtg gtgtgcacgt gtgctctggg 300
ctccgaggct tctccagagc tgggagctgg ctggcgtggc aagggcatgc tctggggcag 360
tgtgtccctc aggaaccagg gtcctccctc ccctttctgc ctggtcagcc ccgtggcctc 420
t 421

<210> 154
<211> 423
<212> DNA
<213> Homo sapiens

<400> 154
ggcatgagtg gaagggaggc agctgccttt gtttgccatg gatgggtagg ggctgcactg 60
agcagcagcg gtgttcttca tccggctgca cccccaacag agctctttct tccccagatc 120
ccttttacag ttggattctc cctcttggat ctggctctgc cttagtccga cctagaggga 180
tcagcttcgc ccacgcccac tctcacccgg aacctttcat ctcttattga agccttttag 240
gcccattggg atgttcatta gaactctgaa aactacagtt ctcccctta tgaggactgc 300
accacagctc gccctctcct gggttccgcc tggttgcaga gtgagcccat gggacagccc 360
tctgaaatta tactgcttac aaccatgctg agtctgcaag gacttccgcc aagcctttcc 420
gtc 423

<210> 155
<211> 312
<212> DNA
<213> Homo sapiens

<400> 155
tctgtcactc acaaaacaca gtgcgcgcac atagcggggg gggagcacac acacaagatg 60
tgtgtgtata caacccgcgc gcgagagagc gctctctttt gtggggggga aaaaaactct 120
tatacacaca cgtgtgtgtg tgtcgctctc cgaaaataca cactataaca aacgcactgt 180
gtgtgtgaga cacacactcc tctctccgag tggggagaga gagatcgcgc tccactctta 240
aacacatatg cgctcacaga gagcatatat atgttttttt tgagagaaga gagagatctc 300
tttgtggttt ct 312

<210> 156
<211> 428
<212> DNA
<213> Homo sapiens

<400> 156
tgaccttcca ggctacctac gcaggtgtcg gggccaacaa gcacctgcag gagctggccc 60
aggaggaggt gaagcagcat gcccaggaac tctgggctgc ctacaggggt ctgctgcgag 120
ttgccttaga gcgcaagggc caggccctgg aggaggatga agacacagag acaagggacc 180
tccaggtgca tggattggtg ctgcccctca tgctgcccag cttctactca gagctcttca 240
cgctctacct gctgcttcat gagcgggagg acagcttcta cagccagggc attgccaact 300
tgagcctctt tcctgatacc caactgctcg agttcctgga tgtgcagaag cacttgtggc 360
ccctcaagga cctcacgctg acgagcaatc agaggtactc cctggtcagg gacaagtgtt 420
tcctgtca 428

<210> 157
<211> 430
<212> DNA
<213> Homo sapiens

<400> 157
ggcacgagag gactttgagc ccagagagat gaagtcattt gctcaaggca gcagtcagtg 60
gaagggcttg gagaaggaga aggggtctga aggtggtgtg ggacacatga gagtgatctc 120
gcagcttggt ttgctgcagc agactcggac aagcattgtt tcagtgcctg gtttctccct 180
ccacttgatg gggccaact ccaacccaat gtcccattcc tatcctgaaa tgcttctaaa 240
ggcagtgccc tgagaaccac caacctcaca gcctgtctcc attttattgt cttctgggaa 300
cttctccctt ctgtctagca cctgtttgca ctgggattgt cctgtctgtc cttcagttgg 360
atcctggttt gcacccgatg aggatttagc aattttaggc tgtgcttcgg caaaggccaa 420
ctcacaatgg 430

<210> 158
<211> 405
<212> DNA
<213> Homo sapiens

<400> 158
ggcacgaggg aagatttcca gtggtctcaa tggtgtgaat cctatgaagg tgtcttattt 60
gttgaattag aggtgaaagc ctccttcctc actctttttt agaaacagtt tagttttatt 120
attatgcaga atttgttgag caaattgcaa cagcccaagc cacagctagc tccacaagag 180
cccttccatg agccctcaac ctgggatctc gtgtatcttt gttggaatgg acattaggtt 240
tccaagtcca ggcctgtgat ttagaagggt caggttgggt aggagagagg agagtcttgg 300
aggggctgct ccatgggggt cacacctctc tcctgtgggt tttcgctggt gattgagttc 360
tgaggcattt gctgcattga ctgttgtagc tttaactcgt gtgca 405

<210> 159
<211> 403
<212> DNA
<213> Homo sapiens

<400> 159

ggcacgagcc tgactcaagg ggttttggaa gatttccagt ggtctcaatg gtgtgaatcc 60
tatgaaggtg tcttatttgt tgaattagag gtgaaagcct ccttcctcac tctttttag 120
aaacagttta gttttattat tatgcagaat ttgttgagca aattgcaaca gcccaagcca 180
cagctagctc cacaagagcc cttccatgag ccctcaacct gggatctcgt gtatctttgt 240
tggaatggac attaggtttc caagtccagg cctgtgattt agaagggtca ggttgggtag 300
gagagaggag agtcttggag gggctgctcc atgggggtca cacctctctc ctgtgggttt 360
tcgctggtga ttgagttctg aggcatttgc tgcattgact gtg 403

<210> 160
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(417)
<223> n = A,T,C or G

<400> 160
gttctgtggg aatagagggt ccctggtgac agggcagggc tagatctgga gcctgcactt 60
ggcctgtgac atactgtctt gtttctgaga atcctcccct acttctctag ttaatctcca 120
gagacttctg tgactactta atcacaaagg aaattttcag gaatattatc aaatactatt 180
ttagaaaaaa aaagagaagg gatttgaatg ttttcagttc agtttagtta tcnnnnnnnn 240
nnnnnnnccc caaactccag aatgggggcc ccccttctt taaccccacc taaaaatttt 300
tcggaggttc agggttggtt ggcaaattac aaaaacccca aaagaaaatg ggggttaacc 360
cccttggaaa agttttctta ctttgggggg tggccctttg acgtnggccc gggttac 417

<210> 161
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

<400> 161
ctatatctct ctgcgccctc tccccctctt gtgttttccc ccgcccctct agagatatct 60
ctctcactcg cgggcgcaca cccccccttta caaaataggg ggctctctgt gtgtggtgtt 120
tttcttgggc gccccctctt tttttttctt tttgcgggcc cccccctgtg tgtctctctc 180
tagacacacc cccccgcgcg tgttttttat aaatatctgt ctctcacaca ccccctactg 240
cccctctgtg tgtgggcgcg ttccccccca cacacacaga gtgtgtgnnn nnnnnnnnnn 300

<210> 162
<211> 411
<212> DNA
<213> Homo sapiens

<400> 162
ggcacgaggg caccgagcct cctgtgggag gtcccgaggc agcttcgcct gctcggcctg 60
gctgcagccc tcacctgccg cagccttagc tgagcagccg ccgccactgg gcgcccccccg 120
ctccccactt cgccagcgcc cgctcctcgg ctcggcccgg ggtagtttgt agggacgcag 180
ctctccacgt gcgcgactgc gaggctggac gctacgggct cctggaaagg agcagacacc 240
agcatttgcc acaatgctgt catccactga ctttacattt gcttcctggg agcttgtggt 300
ccgcgttgac catcccaatg aagagcaggc agaaagacgt ccgcactgag aggattctgg 360
agacccttca cgttggaagg agtgatgctc aaggttagta gaacagatca a 411

<210> 163
<211> 412
<212> DNA
<213> Homo sapiens

<400> 163
gcacgatcca tcattcaatt cggacagcca ctccaactga cctgttccgt ggctgcctcg 60
agagcctccc atagcccagg cctccgtagg cctcctcctg tgtgagtccc accaggagcc 120
acgtgcccgg ccttgccctc aagggttttt gcttttctcc tgtgcacctg gctaggctga 180
aggcgagggg tggaggaggc cccagcacag cctcatctcc atgtgtacac gtgtgtacgt 240
gtgtatgcgt gtgtgtacgc gtgtacgcgt gtgtgtacgc gtgagtacgt gctgtgtgta 300
cacatgcgtg gccgcctgtg gtgtgcacgt gtgctctggg ctccgaggct tctccagagc 360
tgggagctgg ctggcgtggc aagggcatgc tctggggcag tgtgtccctc ag 412

<210> 164
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(411)
<223> n = A,T,C or G

<400> 164
ggcacgagag gatatggtgc aaaaaaatat gattttgtta accacaacaa aaagaaaggt 60
aagaaatgct aggagaaagc taaaagctcc atactaaaat aatggtccta atattaagca 120
aagtaaaatg tggtatgatt ttgagtggtc agcagagtgt aagaataatc tatttgcact 180
tgatactttc agctgtcaca gaggtcatag aattgggctt attgagaagg aaaggtaaat 240
gctagtacac tacttggctc agaagtgaac aaaattgcag tttgnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn n 411

<210> 165
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(415)
<223> n = A,T,C or G

<400> 165
ggcacgagag gatatggtgc aaaaaaatat gattttgtta accacaacaa aaagaaaggt 60
aagaaatgct aggagaaagc taaaagctcc atactaaaat aatggtccta atattaagca 120
aagtaaaatg tggtatgatt ttgagtggtc agcagagtgt aagaataatc tatttgcact 180
tgatactttc agctgtcaca gaggtcatag aattgggctt attgagaagg aaaggtaaat 240
gctagtacac tacttggctc agaagtgaac aaaattgcag tttgnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nngtn 415

<210> 166
<211> 403
<212> DNA
<213> Homo sapiens

<400> 166
ggcacgagga aggtgtcagg agcatcccat ttgtgtctct ctctctacct ctgtgaaggg 60
cgcgaatggg cagagcagaa cttctagaag ggaagatgag cacccaggat ccctcagatc 120
tgtggagcag atccgatgga gaggctgagc tgctccagga cttggggtgg tatcacggca 180
acctcacacg ccatgctgct gaagctcttc tcctctcaaa tggatgtgac ggcagctacc 240
ttctgaggga cagcaatgag accaccgggc tgtactctct ctctgtgagg gccaaagatt 300
ctgttaaaca ctttcatgtt gaatatactg gatattcatt taaatttggc tttaatgaat 360
tctcatcttt gaaggatttt gccaagcatt ttgcaaatca gcg 403

<210> 167
<211> 407

<212> DNA
<213> Homo sapiens

<400> 167
ggcacgaggg gcgacaagct gttggagctg caatgggccg cggctgggga ttcttgtttg 60
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag cccccggaga 120
cagcggcaca gaggtgcttc tgccaggtta gtggttactt ggatgattgt acctgtgatg 180
ttgaaaccat tgatagattt aataactaca ggcttttccc aagactacaa aaacttcttg 240
aaagtgacta ctttaggtat tacaaggtaa acctgaagag gccgtgtcct ttctggaatg 300
acatcagcca gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 360
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaat 407

<210> 168
<211> 416
<212> DNA
<213> Homo sapiens

<400> 168
ggcacgagac acaactttga gacaccccaa gtgctttctg cagaggttgt cgttggaaaa 60
ctgtcacctt acagaagcca attgcaagga ccttgctgct gtgttggttg tcagccggga 120
gctgacacac ctgtgcttgg ccaagaaccc cattgggaat acaggggtga agtttctgtg 180
tgagggcttg aggtaccccg agtgtaaact gcagaccttg gtgctttgga actgcgacat 240
aactagcgat ggctgctgcg atctcacaaa gcttctccaa gaaaaatcaa gcctgttgtg 300
tttggatctg ggctgaatc acataggagt taagggaatg aagttcctgt gtgaggcttt 360
gaggaaacca ctgtgcaact tgagatgtct gtggttgtgg ggatgttcca tccctc 416

<210> 169
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(386)
<223> n = A,T,C or G

<400> 169
ggcacgagga atctcgcctc tgtctggtgt gttacctact gggggcacag gaacaatttc 60
ctcaaggaga cagtggcatg gagctttgaa agacgagtag gtgttagcaa ggaaataagg 120
aggaacgggg gttacgggca gaggagaaag cacatgccaa gtcagcaaag aaaagtagaa 180
ttcgaaaact ttttaaaaat attactaagg attttcacaa tgctgcactg ggctagaaac 240
tgaagctaaa acagatacgt ggtccctgct gctatggggc ttccgttcta gaggcaagga 300
caggttgtga tgagggttct gaaggataga gaccaagcag ggagggtgtt gaggaggctt 360
ctgcgagacc tgaaggatgg gaagcn 386

<210> 170
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 170
ggcacgagaa tagagggtcc ctggtgacag ggcagggcta gatctggagc ctgcacttgg 60
cctgtgacat actgtcttgt ttctgagaat cctcccctac ttctctagtt aatctccaga 120
gacttctgtg actacttaat cacaaaggaa attttcagga atattatcaa atactatttt 180
agaaaaaaaa agagaaggga tttgaatgtt ttcagttcag tttagttatc nnnnnnnnnn 240
nnnnncccaa aactcaagat tggggccccc ccctccttta accccgctaa aaagtttttt 300
gggggtttag ggtgggttgg caaataacaa aacccccaaa agaaaagggg ggtaaacccc 360
cttggaaaag tttcctaact ttgggggcg c 391

<210> 171
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 171
ggcacgagcc tgcatcgacc catttttcct catgacaaac tattggtgca nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnact tagggccact 120
catctgtcat ggaaccagaa tctaaatcca aataggctgt tgccagtaca gatggtaagt 180
acatgtactt ctggcaggaa agcagaataa aagttgactg aacctgaaag tctcggaaat 240
ggtcttctca tttctattct gtaaagtgtc acgtcttcta ggcctacctc tgtcaatatt 300
gaaatacaaa attaactttt tctgcttttt atttcacaaa tcaacgggaa cagtcttagt 360
catttgtgtt ttatgagttt taattaggcc n 391

<210> 172
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(385)
<223> n = A,T,C or G

<400> 172
ggcacgagga cagtggcatg gagctttgaa agacgagtag gtgttagcaa ggaaataagg 60
aggaacgggg gttacgggca gaggagaaag cacatgccaa gtcagcaaag aaaagtagaa 120
ttcgaaaact ttttaaaaat attactaagg attttcacaa tgctgcactg ggctagaaac 180
tgaagctaaa acagatacgt ggtccctgct gctatggggc ttccgttcta gaggcaagga 240
caggttgtga tgagggttct gaaggataga gaccaagcag ggagggtgtt gaggaggctt 300
ctgcgagacc tgaaggatgg gaagccagga agtgggaggg gtgggggtnc aggctggagg 360
ggcccaatgt angtgtaaag ggact 385

<210> 173
<211> 392
<212> DNA
<213> Homo sapiens

<400> 173
ggcacgagaa aggctggaag ggaggcagct gcctttgttt gccatggatg ggtaggggct 60
gcactgagca gcaccggtgt tcttcatccg gctgcacccc cgacagagct ctttcttccc 120
cagatccctt ttacagttgg attctccctc ttggatctgg ctctgcctta gtccgaccta 180
gagggatcag cttcgcccac gcccactctc acccggaacc tttcatctct tattgaagcc 240
ttttaggccc attgggatgt tcattagaac tctgaaaact acagttctcc cctttatgag 300
gactgcacca cagctcgccc tctcctgggt tccgcctggt tgcagagtga gcccatggga 360
cagccctctg aaattatact gcttacaacc at 392

<210> 174
<211> 394
<212> DNA
<213> Homo sapiens

<400> 174
ggcacgagat ggaatgacag cttttttttag tagcatatcc ttgcgctgtg ttagatggag 60
tctttgccct gatttccgtc ttttgaaaat ttatctggga tgtggacatc agtgggccag 120
atgtacaaaa aggaccttga actcttaaat tggaccagca aactgctgca gcgcaactct 180
catgcagatt tacatttgac tgttggagca atgaaagtaa acgtgtatct cttgttcatt 240
tttatagaac ttttgcatac tatattggat ttacctgcgg tgtgactagc tttaaatgtt 300

tgtgtttata cagataagaa atgctatttc tttctgggtc ctgcagccat tggaaaaact 360
tttttctttg gaaataataa ggtttttgat agat 394

<210> 175
<211> 387
<212> DNA
<213> Homo sapiens

<400> 175
ggcacgaggg cagttagggc tgccatgtgc tgggagctgt gtgtctgctc tccttcgtcc 60
gctcccccag ggcagtgtgg tagcacatcc cattgtagag atgagggcac cgaggcttcc 120
tggagcatac cacctggtcc cgttcatgag tggtggcaaa gctagcactc tcacttgtcc 180
attctgcctt cctggagacc agtgggatgg gtcagtacag cccaccacac cattagcccc 240
aggaacataa ggctgtggct agacagcagg ggtctcaggt tcatacatga ggactggctt 300
gtccttgagc acccactcac ctgtctatgt ggggaggaat cctacaatag gtcaccatgg 360
caggctgggg cttgctgacc ctgcccc 387

<210> 176
<211> 395
<212> DNA
<213> Homo sapiens

<400> 176
ggcacgagca gacctccatt acctccatcc ctgttggatt atttaaagaa agcctcagac 60
agtaagggct ttttttaaaa gaataaaatg acttggtttg cgcttggaag caggggaagc 120
attcagatga gcggtttctg cattaaccct gcctatcacg catctcgtgt cctgtgtggc 180
tggcgagccc cccttggaag gttctggtgc ttcagctggc tcctgcagag tccaccccgc 240
ctcgtggtgg gaatgcagag ccctttgctt tccttcttgc cgcctgcttc ctgttcctgg 300
ggacccgctg ggcctttggt ctgcatcccc tggccaggtc cctcagggct gatgcgcgta 360
gaaggacttt gagcagtggt ggcagcactt gccct 395

<210> 177
<211> 388
<212> DNA
<213> Homo sapiens

<400> 177
ggcacgaggg acgctgcgga gcccgctcac ccgctccctg tacgtgaaca tgactagcgg 60
cccgggtggg ccggcggcgg ccgcgggcgg caggaaggag aaccaccagt ggtatgtgtg 120
caacagagag aaattatgcg aatcactcca ggctgtcttt gttcagagtt accttgatca 180
aggaacacag atcttcttaa acaacagcat tgagaaatcg ggctggctat ttatccaatt 240
atatcattct tttgtgtcat ctgtttttag cctgtttatg tctagaacat ctatcaatgg 300
gttgctagga agaggctcaa tgtttgtgtt ttcaccagat cagtttcaga gactgcttaa 360
aattaatcca gactggaaaa cccacaga 388

<210> 178
<211> 397
<212> DNA
<213> Homo sapiens

<400> 178
ggcacgagca ggatccctca gatctgtgga gcagatccga tggagaggct gagctgctcc 60
aggacttggg gtggtatcac ggcaacctca cacgccatgc tgctgaagct cttctcctct 120
caaatggatg tgacggcagc taccttctga gggacagcaa tgagaccacc gggctgtact 180
ctctctctgt gagggccaaa gattctgtta aacactttca tgttgaatat actggatatt 240
catttaaatt tggctttaat gaattctcat ctttgaagga ttttgtcaag cattttgcaa 300
atcagccttt gattggaagc gagacaggca ctctgatggt tctaaaacat ccctacccaa 360
gaaaagtgga agaaccctcc atttatgaat ctgtccg 397

<210> 179
<211> 397
<212> DNA
<213> Homo sapiens

<400> 179
ggcacgaggc gtggggcgac aagctgccgg agctgcaatg ggccgcggct ggggattctt 60
gtttggcctc ctgggcgccg tgtggctgct cagctcgggc cacggagagg agcagccccc 120
ggagacagcg gcacagaggt gcttctgcca ggttagtggt tacttggatg attgtacctg 180
tgatgttgaa accattgata gatttaataa ctacaggctt ttcccaagac tacaaaaact 240
tcttgaaagt gactacttta ggtattacaa ggtaaacctg aagaggccgt gtcctttctg 300
gaatgacatc agccagtgtg gaagaaggga ctgtgctgtc aaaccatgtc aatctgatga 360
agttcctgat ggaattaaat ctgcgagcta caagtat 397

<210> 180
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(399)
<223> n = A,T,C or G

<400> 180
ggcacgaggt caccccttttt gcctccatcc tcaaagacct ggtcttcaag tcatccgtca 60
gctgccaagt gttctgtaag aagatctact tcatctgggt gacgcggacc cagcgtcagt 120
ttgagtggct ggctgacatc atccgagagg tggaggagaa tgaccaccag gacctggtgt 180
ctgtgcacat ctacatcacc cagctggctg agaagttcga cctcaggacc actatgctgt 240
acatctgtga gcggcacttc cagaaggttc tgaaccggag tctattcaca ggcctgcgct 300
ccatcaccca ctttggccgt cccccctttg agcccttctt caactccctg caggaggtcc 360
acccccacgt ccggaagatc ggagtgttta gctgtggcn 399

<210> 181
<211> 402
<212> DNA
<213> Homo sapiens

<400> 181
ggcacgaggc tacttcgctc gcaaggatta gtactgcaag gagtatgtgg cagctgtcct 60
ggagcatatc gagaacaaga acctcatgcc acctcttcta gtggtgcaga ccctggccca 120
catctccaca gccacactct gcgtcatcag ggactacctg gtccaaaaac tacagaaaca 180
gagccagcag attgcacagg atgagctgcg ggtgcggcgg taccgagagg agaccacccg 240
tatccgccag gagatccaag agctcaaggc cagtcctaag attttccaaa agaccaagtg 300
cagcatctgt aacagtgcct tggagatgcc ctcagtccac ttcctgtgtg gccactcctt 360
ccaccaacac tgctttgaga gttactcgga aagcgaagct ga 402

<210> 182
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 182
ggcacgagag caactcaggc ctgctgggtt aactgcttac accattttcc ttcccctcct 60
cttccttgcc ttcgacactc ttaacctgga aaaagcacta atttgtcctc catatctgtg 120
gttttgtcat ttggaaaggt tgtagaaatc ctagagtatg tgacctttta agatgcactt 180
tttagaaaac tcaacatgtt gctcttgtgt taatagtttg ttctttttag tgttcggtat 240
tctcttgtgt ggtcatgccc cagtttattt aaccatccca tagatgttta ttttcccttg 300
taaagttggt tagcatgtan nnnnnnnnnn nnnnnnggga aactcattct cnnnnnnnnn 360
nnnnnnnnnn nnnnntgccc cttg 384

<210> 183
<211> 384

<212> DNA
<213> Homo sapiens

<400> 183
ggcacgaggg aaggtgaggg ctgagaagga ggcatgccag cgggagaaag agctgcctgc 60
agcagtacat cccttccatt ttgtttaaat tgggcttgga gaatctattc tgaaaacatt 120
gactctagac ttgtagaaaa gagccatttt agtttcaact caaatgtaaa gcaaggtagt 180
ttggtgacat tttgctttta tgtgaaatag tgcacagtat gagttaatct gagcaggtct 240
gaattgacca aatgcttatc tacgaggttc ctagagctct gctgaccctt ggccgaaact 300
ctaaaatgta cctattaaag ataaatgctt ctaccaaagt aaaactctgt gagttgtttc 360
agggcagaat gtaccagcca gtca 384

<210> 184
<211> 379
<212> DNA
<213> Homo sapiens

<400> 184
ggcacgagct tcctccagcc tccacagcct tggctcagtg tccctgtgta caagacccag 60
tgacttccag gctcccagaa accccaccct aaccatgggc caacccagaa cacccccactc 120
tccaccactg gccaaagaac atgccagcag ctgcccccca tccatcacca actccatggt 180
ggacataccc attgtgctga tcaacggctg cccagaacca gggtcttctc caccccagcg 240
gaccccagga caccagaact ccgttcaacc tggagctgct tctcccagca acccctgtcc 300
agccaccagg agcaacagcc agaccctgtc agatgccccc tttaccacat gcccagaggg 360
tacgtcgtaa accaatatt 379

<210> 185
<211> 368
<212> DNA
<213> Homo sapiens

<400> 185
ggcacgagac ccggtccagg tgccctacgt cggcgcgagc gcgcggcagg tggagcacgt 60
gttgtcgctg ctgcgaggac gccccggaaa aacggtggat ctgggctctg gcgacggcag 120
gatcgtgctg gcggcccaca ggtgcggcct ccgcccggcc gtgggctacg agctgaaccc 180
ctggctggtg gcgctggcgc ggctgcacgc ctggagggcc ggctgtgccg gcagcgtctg 240
ctatcgccgc aaggatctct ggaaggtaac ctggggatcc ctggccaccc gctgacagcc 300
caaggtgcgg ctgacacctg cgagggctgg gggccgggac tcggaagctg cgatgacccg 360
gtgcccac 368

<210> 186
<211> 375
<212> DNA
<213> Homo sapiens

<400> 186
ggcacgaggt ctcacagagc gagaaggtgt caggagcagc ccatttgtgt ctctctctct 60
acctctgtga agggcgcgaa tgggcagagc agaacttcta gaagggaaga tgagcaccca 120
ggatccctca gatctgtgga gcagatccga tggagaggct gagctgctcc aggacttggg 180
gtggtatcac ggcaacctca cacgccatgc tgctgaagct cttctcctct caaatggatg 240
tgacggcagc taccttctga gggacagcaa tgagaccacc gggctgtact ctctctctgt 300
gagggccaaa gattctgtta aacactttca tgttgaatat actggatatt catttaaatt 360
tggctgtaat gaatt 375

<210> 187
<211> 368
<212> DNA
<213> Homo sapiens

<400> 187
ggcacgaggc cgtgcagagc ctgtatggta agcccctagg gggctcaaag gccggccagc 60
tcccaggaaa gatgtgcact gactttgaaa cctgggactc ctacagcccc caaggaaggc 120
gccctgaaac gcagggccct aaatactgcc actcttcctt cgatgccatc actgtagaca 180

ggcaacagca actgtacatt tttaaaggga gccatttctg ggaggcggca gctgatggca 240
acgactcaga gccccgtcca ctgcaggaaa gatgggtcgg gctgcccccc aacattgagg 300
ctgcggcagc gtcattgaat gatggagatt tctacttctt caaagggggg cgatgctgga 360
ggatccgg 368

<210> 188
<211> 436
<212> DNA
<213> Homo sapiens

<400> 188
ggcacgagaa ggggctgggg tgggctcagg caaggcctgg ggccctggcc ttcttcctgg 60
caggggggagg caggggactg tgcaggggct cagggaggcc tcccccacct gccccctgac 120
cacacccact ctgatgaggc tcatggcctc ctggcaggtc gacggaggag atcatcgccc 180
tcttcatttc catcacgttt gtgctggatg ccgtcaaggg cacggttaaa atcttctgga 240
agtactacta tgggcattac ttggacgact atcacacaaa aaggacttca tcccttgtca 300
gcctgtcagg cctcggcgcc agcctcaacg ccagcctcca cactgccctc aatgccagct 360
tcctcgccag ccccacggag ctgccctcgg ccacacactc aggccaggcg accgccgtgc 420
tcagcctcct catcat 436

<210> 189
<211> 435
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(435)
<223> n = A,T,C or G

<400> 189
ggcacgagac agaccctttc ttcctaaagg ctttgtggca tcagacacat aaagggtata 60
tgtagtgtgg agcactaacc atggcagggt aatttattcc aggcacagag tcataattct 120
ggaaacatct agactcactg cattaacaga gcattttgtt tctaaagtag acctcttatg 180
tcatccagat ttcactcatt ctgaccacag ccaggaagct gagggtgaag ccagaattag 240
ctgaaaccca ccaagagctg catagagcac gtttagctag agtaggagtt tgcagtgctc 300
atatgggaaa tgctgctgct atacttttag gaatttctga gtgcaattta gaaacatcta 360
gcacacttga aacactgcgt atcattntcc tcactcatga atatagtcat cagaattcat 420
aaatagttta cctga 435

<210> 190
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(437)
<223> n = A,T,C or G

<400> 190
ggcacgagat taggaccctt ccttggcaca ggggtgagaa agagcttggg gaacgcttgg 60
cattatggag ggctggaagg ggctcaaccc cgatttggag agaagtttgg gatggagtgg 120
gcgagagatt gagagagcga gcaggaaaag aggtcttgga gcctgggact gatggtggat 180
aaggcctgga aagaagatga cgaggaggag gagagaggga agtggggtgg atgaggagca 240
ggctgacacc tgggctgccc tcaatcccca aggccaggga gggcggngct ggcccctggg 300
aagaactggg tctctgggct ccctatgcac tgcccaaact ggctgagcca ggagtggggc 360
aggaagtgag agtcaaggcc cagcaaaagg agggggagga gctgccaatt ataaccttgt 420
gganggaccg gtttgng 437

<210> 191
<211> 434
<212> DNA

<213> Homo sapiens

<400> 191
ggcacgagaa gaaactgtga agggaaagaa aggtttatac tgagaaatgg aagagataat 60
tttagaaact tgtgaaaaat ggcttaatct aaatgagtgt taggggagat acagttgtga 120
tgataggttg agctcacatg gtggagagcc acagttgcgg gtgcttgcac tgataatgtg 180
agggcatgga gacagacaat aggttgaatg ctcttttttt acaaaaggaa gtagaaaggg 240
agggggatgt aaatttgata aataggttgg tgaaaactta tattttcttg taaagagaga 300
gaactgagca tgttgtaggt ataaggtaaa aaggcgtgaa gaggaatatt tcgttgataa 360
tgaaagtgag cagctaggga agaaaactcc cagaggaaga gggaggcaag gaaatcaaga 420
acacacttaa agtg 434

<210> 192
<211> 323
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(323)
<223> n = A,T,C or G

<400> 192
gggtctctcg ccccctctc tctcttttgt gtgtctctct ctctgtcccg tgtgtgnnnn 60
nnnnnnnnnt ctctctatat ctcgcgcgcg cgcactcccg tgtgtgtgtg tgaccccgcc 120
ccctcatgcg ctctctcatt tgtggagaga gagaccgcta tctatctctc tctccccgc 180
cctatacaca tctccctctc tgtgaaagag acgtgtgtgt gtctccacac cccttgggcg 240
cgcgcgcgcc accccctctc ctgggggggg tgtcctctct gtatatatat atgtgcacac 300
acgcgcgcgc gctctgtgtt gtt 323

<210> 193
<211> 412
<212> DNA
<213> Homo sapiens

<400> 193
ggcacgagaa ggggccgtga cagccgttgc catctgctgc cggagccggc acctggcgca 60
ggcctcccag gagctccagt gacagcccca tcccaggatg ggtgtctggg gagggtcaag 120
ggctggggct gagctttaaa atggttccga cttgtccctc tctcagccct ccatggcctg 180
gcacgagggg atggggatgc ttccgccttt ccggggctgc tggcctggcc cttgagtggg 240
gcagcctcct tgcctggaac tcactcactc tgggtgcctc ctccccaggt ggaggtgcca 300
ggaagctccc tccctcactg tggggcattt caccattcaa acaggtcgag ctgtgctcgg 360
gtgctgccag ctgctcccaa tgtgccgatg tccgtgggca gaatgacttt ta 412

<210> 194
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(405)
<223> n = A,T,C or G

<400> 194
cgttgctgtc ggtcagcaat gaaataaata tcttgtagaa tgttcnnnnn nnnnnnnnnn 60
nngaaccctc gggggccctt ttttcccgaa acccccactg gaaaaaaacc cttggggggt 120
tggcaaaacc ccccaataaa aggggggggaa aaaaaggctt tttttggaaa aatggggggg 180
tctttgcttt ttttggaccc ctttaaagcg gggaaaacca ggttaacccc ccccaggggc 240
nnnnnnnnnn gtttcagggc cnnnnnnnnn nnnnnnnnnt tttttccctn tctcccttct 300
gtctcgccct gctgcgctgc cgttttctcg ttccactccc cccgtttttg tactcccccc 360
gtgccgttga gcgtccaccc tattctttcg cgccggtgca ccccc 405

<210> 195
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(400)
<223> n = A,T,C or G

<400> 195
ggcacgagat taggaccctt ccttggcaca ggggtgagaa agagcttggg gaacgcttgg 60
cattatggag ggctggaagg ggctcaaccc cgatttggag agaagtttgg gatggagtgg 120
gcgagagatt gagagagcga gcaggaaaag aggtcttgga gcctgggact gatggtggat 180
aaggccttga aagaagatga cgaggaggag gagagaggga agtggggtgg atgaggagca 240
ngctgacacc tgggctgccc tcaatcccca aggccaggga gggcggngct ggcccctggg 300
aagaactggg tctctgggct ccctaggcac tgcccaaact ggctgagcca ggagtggggc 360
aagaaatgag agttcaggcc caacacaagg agggggaggg 400

<210> 196
<211> 402
<212> DNA
<213> Homo sapiens

<400> 196
ggcacgagat taggaccctt ccttggctca ggggtgagaa agagcttggg gaacgcttgg 60
cattatggag ggctggaagg ggctcaaccc cgatttggag agaagtttgg gatggagtgg 120
gcgagagatt gatagagcga gcaggaaaag aggtcttgga gcctgggact gatggtggat 180
aaggcctgga aagaagatac taggaggagg agagagggaa gtggggtgga tgaggagcag 240
gctgacacct gggctgccct caatccccaa ggccagggag ggcggggctg gcccctggga 300
agaactgggt ctctgggctc cctaggcact gcccaaactg gctgaaccag gagtggggca 360
agaagtgaga gtcaaggccc aacaaaagga gggggaggag ct 402

<210> 197
<211> 401
<212> DNA
<213> Homo sapiens

<400> 197
ggcacgagct ctcagcggcc ggtttctgcg tccgctgccg caggttccac cgcgctccag 60
gtattttttt ttctgaagga aagctgcttc ctcatatgtt tcaagaatgg ctctccctat 120
cattgtaaaa tggggtggac aggagtattc agtgaccaca ctttcagaag atgatactgt 180
gctcgatctc aaacagtttc tcaagaccct tacaggagtt cttccagaac gccaaaagtt 240
acttggactc aaagttaaag gcaaacctgc agaaaatgat gttaagcttg gagctctcaa 300
actgaaacca aatactaaaa tcatgatgat gggaactcgt gaggagagct tggaagatgt 360
cttaggtcca ccccctgaca atgatgatgt tgttaatgac t 401

<210> 198
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(397)
<223> n = A,T,C or G

<400> 198
tgcatattag acattcttaa cagggcggca gtctagtgtt gaaagtttta tttttccatt 60
tttcttttaa gcaaattttt tttaaaaaat tctgattnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn tctgatttaa 240
ttcttttatt tatcataagg ggtttaattc ctgaagtaaa ggtttgcacc tattaaactt 300

aaaactgcca aatgattttt gttcttttat gtgcgcgata gaaatacaaa gaatggagtg 360
gccacctcct ccctttcaag ctagggcagc agggacg 397

<210> 199
<211> 398
<212> DNA
<213> Homo sapiens

<400> 199
ggcacgagaa gaaaggttta tactgagaaa tggaagagat aattttagaa acttgtgaaa 60
aatggcttaa tctaaatgag tgttagggga gatacagttg tgatgatagg ttgagctcac 120
atggtggaga gccacagttg cgggtgcttg cactgataat gtgagggcat ggagacagac 180
aataggttga atgctctttt tttacaaaag gaagtagaaa gggaggggga tgtaaatttg 240
ataaataggt tggtgaaaac ttatattttc ttgtaaagag agagaactga gcatgttgta 300
ggtataaggt aaaaaggcgt gaagaggaat atttcgttga taatgaaagg gagcaactta 360
gggaaaaaaa cttcccaagg aggaggggag cagggaaa 398

<210> 200
<211> 394
<212> DNA
<213> Homo sapiens

<400> 200
ggcacgagca gaaggcagcg gtctaggcga ggacgcccgg ctggaccagg agaccgccca 60
gtggctgcgc tgggacaaga attccttaac tttggaggca gtgaaacgac taatagcaga 120
aggtaataaa gaagaactac gaaaatgttt tggggcccga atggagtttg ggacagctgg 180
cctccgagct gctatgggac ctggaatttc tcgtatgaat gacttgacca tcatccagac 240
tacacaggga ttttgcagat acctggaaaa acaattcagt gacttaaagc agaaaggcat 300
cgtgatcagt tttgacgccc gagctcatcc atccagtggg ggtagcagca gaaggtttgc 360
ccgacttgct gcaaccacat ttatcagtca gggg 394

<210> 201
<211> 391
<212> DNA
<213> Homo sapiens

<400> 201
ggcacgagca ggcgtgtctg ggtaaccatg tggctcctgc tggcctcccc tgcctgtccc 60
caaagcacag ggctcagctc cagagggaga cgggctgggc tgtcagtggt cccaggtgca 120
tcccactttc cagcagcact tggtgccagc agaggctgca ggtgtggcag gagggggccc 180
agccgtgagg gcaccaggtt caggcccggc atctcagggt ggagagccag ggctgtcctg 240
aacctccaga gggggtgagc tgggaacttg tgtgaagggg ctttttccaa aaggaaaacg 300
ggagcttact ggctcacggc tgatgcccca gacagcctcg aggatctgca ggtccccaga 360
caccaagcct gggtgctctc cagcagacgg c 391

<210> 202
<211> 392
<212> DNA
<213> Homo sapiens

<400> 202
ggcacgagat tctcagtaca ctaaacactt gttaagagtg ttgttaagag ccagagtgag 60
tatcatgtgg gacacagacc ctttcttcct aaaggctttg tggcatcaga cacataaagg 120
gtatatgtag tgtggagcac taaccatggc agggtaattt attccaggca cagagtcata 180
attctggaaa catctagact cactgcatta acagagcatt ttgtttctaa agtagacctc 240
ttatgtcatc cagatttcac tcattctgac cacagccagg aagctgaggg tgaagccaga 300
attagctgaa acccaccaag agctgcatag agcacgttta gctagagtag gagtttgcag 360
tgctcatatg ggaaatgctg ctgctatact tt 392

<210> 203
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 203
ggcacgagga ggagcccgcc ccggaggctg aggctctggc cgcagcccgg gagcggagca 60
gccgcttctt gagcggcctg gagctggtga agcagggtgc cgaggcgcgc gtgttccgtg 120
gccgcttcca gggccgcgcg gcggtgatca agcaccgctt ccccaagggc taccggcacc 180
cggcgctgga ggcgcggctt ggcagacggc ggacggtgca ggaggcccgg gcgctcctcc 240
gctgtcgccg cgctggaata tctgccccag ttgtcttttt tgtggactat gcttccaact 300
gcttatatat ggaagaaatt gaaggctcag tgactgttcg agattatatt cagtccacta 360
tggagactga aaaaactccc cagggtctct cn 392

<210> 204
<211> 386
<212> DNA
<213> Homo sapiens

<400> 204
ggcacgagaa gccttaaacc gggaaatttc catgctatct agaggttttt gatgtcatct 60
taagaaacac acttaagagc atcagattta ctgattgcat tttatgcttt aagtacgaaa 120
gggtttgtgc caatattcac tacgtattat gcagtattta tatcttttgt atgtaaaact 180
ttaactgatt tctgtcattc atcaatgagt agaagtaaat acattatagt tgattttgct 240
aaatcttaat ttaaaagcct cattttccta gaaatctaat tattcagtta ttcatgacaa 300
tattttttta aaagtaagaa attctgagtt gtcttcttgg agctgtaggt cttgaagcag 360
caacgtcttt caggggttgg agacag 386

<210> 205
<211> 295
<212> DNA
<213> Homo sapiens

<400> 205
gcgctctctt cacacacaaa agatatatat atagaaaggg agtgtggata tcccccctaa 60
atatgtgagc gtgtctctct cgaccgtctc ccccagagaa aatatctcta gagagagcac 120
aagtgtgttc tctgtgtctt gtgtgtgaga aaaaataagt gcccgcgcac acatagattt 180
ttatatcgct cccccccgcg cctttatata tgtttttggt gtgtatatat attttataca 240
aaaacatgtt tctttttgag gccccttaca acaaaaattt tgttcttttt gaacc 295

<210> 206
<211> 383
<212> DNA
<213> Homo sapiens

<400> 206
ggcacgaggt tacccatcag cccttgcaag tcccccactc aggcctctgg aaggtccagg 60
gatgggctct gatgagaggg taaaagatgc tcagggaaac acaggcctca gctgcctaga 120
ggaccctccc cctgccttgc agtgggctcg ggtagagcag tatcaggagc tagggttgtc 180
tgctgcccac actcctgctt tttgggatat ctaactgcta aggagggagt tgacatcccc 240
cttctggctc atgtgtctga caccaacaac atggtctctg tccctctctc tttgactctc 300
cctttgtcct ccccatagag ctggggtggg gtggatccct atacctgggg caggcagccc 360
caaagtgggg gagggggatg gca 383

<210> 207
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(385)
<223> n = A,T,C or G

<400> 207
ggcacgagct tcaggataag aagctcatgg ccatgttcct agagtataac aaagccatcc 60
ggaactacac ccgcttcgat gactggtacc tgtgggttca gatgtacaag ggactgtgt 120
ccatgccagt cttccagtcc ttggaggcct actggcctgg tcttcagagc ctcattggag 180
acattgacaa tgccatgagg accttcctca actactacac tgtatggaag cagtttgggg 240
ggctcccgga attctacaac attcctcagg gatacacagt ggagaagcga gagggctacc 300
cacttcggcc agaacttatt gaaagcgcaa tgtacctcta ccgtgccacg gnggatccca 360
ccctcctaga actcggaaga gatgg 385

<210> 208
<211> 374
<212> DNA
<213> Homo sapiens

<400> 208
ggcacgagcc tcagctgcct agaggaccct ccccctgcct tgcagtgggc tcgggtagag 60
cagtatcagg agctagggtt gtctgctgcc cacactcctg ctttttggga tatctaactg 120
ctaaggaggg agttgacatc cccctctgg ctcatgtgtc tgacaccaac aacatggtct 180
ctgtccctct ctctttgact ctccctttgt cctccccata gagctggggt ggggtggatc 240
cctatacctg gggcaggcag ccccaaagtg ggggaggggg atggcagaga ctgtaaaggc 300
gccactggac tctggcaagg cctttattac ctttactccc ctccctctcc catcaccagc 360
ctcaaggcct gagg 374

<210> 209
<211> 425
<212> DNA
<213> Homo sapiens

<400> 209
ggcacgagcc caagtgcttt ctgcagaggt tgtcgttgga aaactgtcac cttacagaag 60
ccaattgcaa ggaccttgct gctgtgttgg ttgtcagccg ggagctgaca cacctgtgct 120
tggccaagaa ccccattggg aatacagggg tgaagtttct gtgtgagggc ttgaggtacc 180
ccgagtgtaa actgcagacc ttggtgcttt ggaactgcga cataactagc gatggctgct 240
gcgatctcac aaagcttctc caagaaaaat caagcctgtt gtgtttggat ctggggctga 300
atcacatagg agttaaggga atgaagttcc tgtgtgaggc tttgaggaaa ccactgtgca 360
acttgagatg tctgtggttg tggggatgtt ccatccctcc gttcagttgt gaagacctct 420
gctct 425

<210> 210
<211> 396
<212> DNA
<213> Homo sapiens

<400> 210
ggcacgagga gcaaggaagt aatattgtca tatttgcagt tgagaatgat ccctgagtct 60
cggtttttctt atctatgaaa tgaggctaag aataataaaa tagagaatta aatgagataa 120
tgcctgtaaa cagtgcctgg catatagctt attattcatc cagctaagag gcccttccat 180
atgtgaagct ttgctctgtg aggtctgtat tacaatcaca ttcagttata gctaattatt 240
tacttatgta gctatctctg aaacttagaa atgaaatcat cgaggaaaaa ggccatttct 300
tgatcctgtc tgtgttccct gttcccagca taaagcctaa cacgtattag gctaatgtca 360
ccgagcaaag aaagcatcaa agtggcgggt cgggcc 396

<210> 211
<211> 267
<212> DNA
<213> Homo sapiens

<400> 211
tctctagaga cacacagaga gggtgagcgg ctctctcaca cgcaccccag agtcaggcgc 60
gcacgctctc tctctctctc tctatccctc agaaagatct tcctttttcc ctctccctgt 120
gatgtagtga gagtttgatg catatttgtc cgtgtccgcc cccacagacc ctctacctct 180
ctgtgctggc cctatcttgt gtgtatgttt ccctctctct ctcgcgcgcc cacacgatgt 240
actttcttta tatgtagtgc cagttcc 267

<210> 212
<211> 396
<212> DNA
<213> Homo sapiens

<400> 212
ggcacgagcc aggaggaccc tcgcttcctc tccgccatgc ttgccacctc ttgcttctga 60
gagtccatct cagttcgcag ttctgtgact tgcattgacc tggctccaat caagctacaa 120
ctcaagcagt cacggggaga aggattgtag atgggccagt gactcacagg gtcaggcact 180
cggggggagcc tgagtcagga ggtcagtggg ccctggaagg gaggggggcaa gcctgggtgg 240
gtaaggttct gggccccagg caagaaggca gagtttctcc gcaggggtgt gtgcaagagc 300
tagctgcgca gaaggtctcc gctggctctc caagccgggc ttgtgaaata ggaacgccaa 360
catcctcctc cacaggcagt ggcaggcacc tcctcc 396

<210> 213
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

<400> 213
tgggctgtct cgcccctcct ccctctctct ttgtactcac agtgaaaaat tatagtgttc 60
gcgtgcgggg cgcgctcttt acttttttttt ctctctcaca catatttata tatatagaga 120
gagcctccga gcgctctgcc cccctcctct ctctctctct tcacgtgtgt gcatcaccca 180
ctcnnnnnnn nnnnctcttc cagagatacg ggggcttgtt tcctccgctc tctctcacac 240
gtctgtgcag cagaggacta tttttttctt tcccccgcgt ctcn 284

<210> 214
<211> 440
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(440)
<223> n = A,T,C or G

<400> 214
ggcacgaggg attgcagtca gcactttctg aatgttttca cacagtatgc aaagcttaca 60
tcataccaag gagtggagag ttgaagtttc ctcccagtga ctccagtgac agaccacacc 120
tagaaagcgt ttctcttcct gagtatttca aaaagatgta aaagagctgg ggagagtatg 180
ggaagaaaca atacaggatt gcctttaatt aattaagaat tgcctcctga taaaaggaaa 240
aagaaattaa tgctggagta tggaggggtg ataaccttaa agattataaa tatttgttgt 300
ctataaatac ttataaatta taaacacaat ataattaaaa ttagaacatc aggaaaagaa 360
ttaaaatcct caggttgcaa aaccaaaatg ttaaccaaaa caaatactca tgagattcaa 420
ctttgttcac ctatagaaan 440

<210> 215
<211> 439
<212> DNA
<213> Homo sapiens

<400> 215
ggcacgagtg cacaggggac acttacggac acagaaatgc acaggggagg ccgagcataa 60
ccaggggtga ggggcaggca gcagttgtag ttactgccgc ggggcactgc tatgtgcagg 120
gacagccagc acccagccca tcaccactcc ctgggctggc tggcaggtat ggcaccctgg 180
gagcccggca tatacccagg gcacccctac ggctgccgcc agtctcatgc ccaggtgggt 240
gctctgggct ggagcgaggg ccaggttttg ggccgaggct tccccaggca atcctgtgag 300
ctcccttcta gcctctgacc cagtctggtc tggcttgcat ggatgtaggg cttggggtgg 360

gaagttcagg tcctggcttt gcctttgcct gatgtggatg agcagctcac atgctcaggg 420
ccacctgaga ctgtcactg 439

<210> 216
<211> 392
<212> DNA
<213> Homo sapiens

<400> 216
ggcacgagga gacagagaag tttggccagg gggtccacca tactgctggt caggttggga 60
aggaggcaga gaagtttggc caggtgggga aggaggaaga cagagtggtc caaggcctcc 120
atcatggcgt tagtcaggct ggaagggagg cggggcagtt tggccacgac attcaccaca 180
cagcagggca ggctgggaaa gagggagaca tagcagttca tggtgtccaa cctggggtcc 240
acgaggccgg gaaggaggca gggcagtttg gccagggagt tcaccatacc cttgaacagg 300
ccgggaagga agcagacaaa gcggtccaag ggttccacac tggggtccac caggctggga 360
aggaagcaga gaaacttggc ccaggggtca ac 392

<210> 217
<211> 394
<212> DNA
<213> Homo sapiens

<400> 217
ggcacgagcc catctggggc agcaccacgt ggatctctcc ctcgtcacct tcaactggtt 60
cctcgtggtc tttgcggaca gtctcattag caacatcctc cttcgggtct gggatgcctt 120
cctgtacgag gggacgaagg tggtgtttcg ctatgccttg gccattttca agtacaacga 180
gaaggagatc ttgaggctac agaatggcct ggaaatctac cagtacctgc gcttcttcac 240
caagaccatc tccaacagcc ggaagctgat gaacatcgcc ttcaatgaca tgaacccctt 300
ccgcatgaaa cagctgcggc agctgcgcat ggtccaccgg gagcggctgg aggctgagct 360
gcgggagctg gagcagctta aggcagagta cctg 394

<210> 218
<211> 432
<212> DNA
<213> Homo sapiens

<400> 218
acacccactt gtttgaggac accatcgatt cgaattcggc acgagcctag ccagcccctg 60
acgtgcctta caggagttct tccagacacg ccaaaagtga cttggactca aagttaaagg 120
caaacctgca gaaaatgatg ttaagcttgt agctctcaaa ctgaaaccac atactaatat 180
catgaggatg gcatctcgag aggagagctt ggaagatgtc ttaggtccac cccctgacaa 240
tgatgatgtt gttaatgact ttgatattga agatgaagta gttgaagtag aaaataggga 300
agaaaaccta ctgaaaattt ctcgcagagc gaaagagtac aaagtggaaa ttttgaatcc 360
tcccagggaa gggaaaaagc ttttggtgct agatgttgat tatacattat ttgaccacag 420
gtcttgtgca ag 432

<210> 219
<211> 395
<212> DNA
<213> Homo sapiens

<400> 219
ggcacgagcc ctttactcct ctacccaaga tcttgcttgt ttctttctaa gttgcctctc 60
tatctagctt gcaggatttg agttgaggaa aacacagact tccatgagtt tgggaactac 120
gagagaaaag acagacagag tcaaatctac agcatatctc tcacctcagg aactggaaga 180
tgtattttat caatatgatg taaagtctga aatatacagc tttggaatcg tcctctggga 240
aatcgccact ggagatatcc cgtttcaagg ctgtaattct gagaagatcc gcaagctggt 300
ggctgtgaag cggcagcagg agccactggg tgaagactgc ccttcagagc tgcgggagat 360
cattgatgag tgccgggccc atgatccctc tgtgc 395

<210> 220
<211> 487
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

<400> 220
tgctcttttg atgatgccat cgattcgaat tcggcacgag cagctagctc agttcaaggt 60
ggaaatggct taacgagagg aacggcaaca gcaggtggct gaggactacg agctcagact 120
ggcccgggag caagcgcgag tgtgcgaact gcagagtggg aaccagcagc tggaggagca 180
gcgggtggag ctggtggaaa gactgcaggc catgctgcag gcccactggg atgaggccaa 240
ccagctgctc agcaccactc tcccgccgcc caaccctcca gctcctcctg ctggaccctc 300
cagccccggg cctcaggagc ccgagaagga ggagaggagg gtctggacta tgcctcccat 360
ggccgtggcc ctgaagcctg tattgcagca gagccgggaa gcaagggacg agctacctgg 420
agcgcctcct ggtttttgca gntcctcctc agatcttagc ctcctggtgg gcccctcttt 480
tcagagc 487

<210> 221
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(365)
<223> n = A,T,C or G

<400> 221
ggatgccagt ggtgaggctg taagcgaaac tcttcagttt aaagctcaag atctcttaag 60
ggcagtccca agatccagag cagagatgta tgatgacgtc cacagcgatg gcagatactc 120
cctcagtgga tctgtagctc actctagaga tgccggaaga gaaggcctga gaagtgacgt 180
atttccaggg ccttccttca gatcaagcaa cccttccatc agtgatgaca gctactttcg 240
caaagaatgt ggccgggatc tggaattttc tcactctgat tctcgggacc aggtcattgg 300
ccaccggaaa ttggggcatt tccgttctca ggactggaaa tttgcgctcc gtggttcttg 360
ggaan 365

<210> 222
<211> 376
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(376)
<223> n = A,T,C or G

<400> 222
ggcacgagga gatttcccgg cgggtcccgg cctctgcgtg cacgcgcctg cgtgctcgcg 60
ctcgcggttc tggcgctgct nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnntgatggc agcagtggcc tgcctgaagc agccactgcc aagaatctag 240
ctgcagtnnn nnnnnnnnnn nnnnnnnnca tgctccacac agccaccgga agccaagaac 300
gcaccctcct gggtacagct gcaagccgcc agccgaggct gcggacccgg gcctccctgg 360
tgctctgggg gttggg 376

<210> 223
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(399)
<223> n = A,T,C or G

<400> 223
ggcacgaggg gtgacagagc ggctggcgca tgctcagtag agcagcctac ggcaagcagc 60
ctccctcagg gaacatcaca ggaagcagct gcaggacctg agtggacagc accagcagga 120
gctggccagt cagctagctc agttcaaggt ggaaatggca gaacgagagg aacggcaaca 180
gcaggtggct gaggactacg agctcagact ggcccgggag caagcgcgag tgtgcgaact 240
gcagagtggg aaccagcagc tggaggagca gcgggtggag ctggtggaaa gactgcaggc 300
catgctgcag gcccactggg atgaggccaa ccagctgctc agcaccactc ttccgccgcc 360
caaaccttca gcttcttctg cttgaccctc cagccccgn 399

<210> 224
<211> 402
<212> DNA
<213> Homo sapiens

<400> 224
ggcacgaggg cagttcagta tcgatggaca gatcttccta ctctttgact cagagaagag 60
aatgtgggca acggttcatc ctggagccag aaagatgaaa gaaaagtggg agaatgacaa 120
ggatgtggcc atgtccttcc attacatctc aatgggagac tgcataggat ggcttgagga 180
cttcttgatg ggcatggaca gcaccctgga gccaagtgca ggagcaccac tcgccatgtc 240
ctcaggcaca acccaactca gggccacagc caccaccctc atcctttgct gcctcctcat 300
catcctcccc tgcttcatcc tccctggcat ctgaggagaa tcctttagag tgacaggtta 360
aagatgatac caaaaagccc ctgtgagcac ggtcttgatc ag 402

<210> 225
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(270)
<223> n = A,T,C or G

<400> 225
ctctctttct ttctccctcc ccccccgggc gcgctcattt atctcgtctc ttatgtctct 60
ctctctgtgt ctgtgacaga cacactcttt ttcatatagc gcgctccctt ttctttgctc 120
tcgggggggg tctctctgta cgcgtgtgtt ctctctccag tgagtgtgca cgcctaggtg 180
agagagagtn nnnnnnnnnn nnnnntgtgt gtgaatttta tatatttcta tatctctcac 240
tctctgggtg tcacactctc cgtgtgtggg 270

<210> 226
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

<400> 226
ggcacgagaa ccctcccagg ctaagcccca atttggggct cgcctgccct gcatcaggga 60
gacatgtcag ctgaggagta attgaccaga tttctgcttt agaaatatgg cagtggaggc 120
aggagatggc atctgaggcc caggctgggg agaagggtgc tgggatgaga acctggagtt 180
cagaccaggg aagggatgag agcctaagaa gaggagctct caccctgaga caggctggtg 240
caggagtctg ctcgatccag gcctgggtcc ctggttccct ctgagcttgg gaggactatg 300
tgagacagaa caggaccagg ggcctgcatt ccccttgta ttattcatct tcnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnn 404

<210> 227

<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

<400> 227
ggcacgagaa gtcactcaac ctctctgagc cttttcttca cctataaagt ggggatagta 60
actacctacc ttatggaagc atatgaggat tgtgtgaaat catccatgta gcccttccac 120
cgccacgtgg agtttggcat ggagcagttt ctaaatggaa gtcatcttga tcaggtgggc 180
tgccaacctc tctgagcctc agtttgctct tctagggaat ggggacaatg caatgggaat 240
ctgaggattg tgtgaaattg tgcaaatgca tgaatgtggg ctgggatagt aaaagggagg 300
gccccggagc agcccacctg ggtcctatc tagtggacgc gcccggtgcc cacccattgc 360
tgtgatgcca gcagcccact gcaagcatn 389

<210> 228
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 228
ggcacgagct gccacctcta gaaagctgct ttcttctatc accgcttgcc cttgaattat 60
tccctgaatg aagccaagaa ccctcccagg ctaagcccca atttggggct cgcctgccct 120
gcatcaggga gacatgtcag ctgaggagta attgaccaga tttctgcttt agaaatatgg 180
cagtggaggc aggagatggc atctgaggcc caggctgggg agaagggtgc tgggatgaga 240
acctggagtt cagaccaggg aagggatgag agcctaagaa gaggagctct caccctgaga 300
caggctggtg caggagtctg ctcgatccag gcctgggtcc ctggttccct ctgagcttgg 360
gaggactatg tgagacagaa cagn 384

<210> 229
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(292)
<223> n = A,T,C or G

<400> 229
ggtgtctctc tctcgggggg gcccccccctc tctctatttt tttttgcgcg cacactcact 60
ctctctctct tttttccccc gcgcgcgcgc acgcgctttt tttttctttt ttctnnnnnn 120
nnnnnactct ctctcttttc tcttttgtgt gggggtctcc ggcgcgcttc tctctctctc 180
tctcacccac agacactctc tctgtgtgcg cacctctctc tctcgggggg ccggatctct 240
ctcccccctc tctatctctg ttattttggg ggtcccctcc gcgctctcct ca 292

<210> 230
<211> 400
<212> DNA
<213> Homo sapiens

<400> 230
ggcacgaggt gggacagaag tagaagaggg tgaatggccc tggcaggcta gcctgcagtg 60
ggatgggagt catcgctgtg gagcaacctt aattaatgcc acatggcttg tgagtgctgc 120
tcactgtttt acaacatata agaaccctgc cagatggact gcttcctttg gagtaacaat 180

aaaaccttcg aaaatgaaac ggggtctccg gagaataatt gtccatgaaa aatacaaaca 240
cccatcacat gactatgata tttctcttgc agagctttct agccctgttc cctacacaaa 300
tgcagtacat agagtttgtc tccctgatgc atcctgtgag tttcaaccag gtgatgtgat 360
gtttgtgaca ggatttggag cactgaaaaa tgatggttac 400

<210> 231
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(332)
<223> n = A,T,C or G

<400> 231
tatatagaca ccccgccttt tttctctctc tctctataca cacaccgtct ctctcccccg 60
tgtgtctctc ccctctcttt tgctcatact tatatacatc tacacacttg tgtgggggac 120
tctctctagc gctccctctc ttttgtgtgg gcgctctcac acacacacac nnnnnnnnnn 180
nnggagactc ctttctctgt ggagaatatg tgtgcgcacc atctctctct ctcttatttt 240
tccctcgcgc gcgcgctctg tgagagagac tctctgttct cacacatatg atatatatat 300
ccctcccctc tctcacactc gtgccccgcg cn 332

<210> 232
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(407)
<223> n = A,T,C or G

<400> 232
ggcacgagaa ctccggctac gtttgctgtc ccaacaaata gaccagggtt ccctaagtgt 60
cgcttcctcc aagaagccct ccctgatgag ttgagccact ttagtttgtg ctcaggctca 120
ccctgcacgt cttggttgct ctcatcactg taatgatcta aaacacacgt ctgctcatga 180
gacccgcatc ccaccccccga tgctggggcc gctcttggat tttcatgcct gctgccagca 240
cccaggggga gctccggaaa tgtctgctgg gggctcggaa tacccacctt tctggtaatg 300
cagcccagcg ggtcccagcc tcgttttcca gccctcactc anaatggagt cgctctggtt 360
cgaacgcctc tgancagtgt gtacctacgt gtcaggccca tccttcc 407

<210> 233
<211> 406
<212> DNA
<213> Homo sapiens

<400> 233
ggcacgagga aagacccacg tgctgcctca tgtggccgac atcctcagca agtcttgccc 60
ggcacccagg tgagcctctg gtgggggtgg gtagtcacca ctcggctctg gaggatgagg 120
cctgggccat aatccagttg cagggacgga tgatctccat ctcgaaggtc ccagaggtaa 180
ctgcgttgtc ccatcctcca ggcatcccct gcggcgctgg ccaagtgcgt gctggccgag 240
gtcccgaagc aggtggtgga gtactacagc cacagaggcc tgccccccgag aagcctgggt 300
gtccctgccg gagaggccag cccaggctgc acaccgtgaa aatgtggagg gcgtaaaggg 360
ggggcccaga aagaaagtgt cccacacaac ctctgtttgc acatgg 406

<210> 234
<211> 380
<212> DNA
<213> Homo sapiens

<400> 234
ggcacgagga gggtgaatgg ccctggcagg ctagcctgca gtgggatggg agtcatcgct 60

gtggagcaac cttaattaat gccacatggc ttgtgagtgc tgctcactgt tttacaacat 120
ataagaaccc tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 180
aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca catgactatg 240
atatttctct tgcagagctt tctagccctg ttccctacac aaatgcagta catagagttt 300
gtctccctga tgcatcctat gagtttcaac caggtgatgt gatgtttgtg acaggatttg 360
gagcactgaa aaatgatggt 380

<210> 235
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(410)
<223> n = A,T,C or G

<400> 235
ggcacgagct gagcaggact tagaggaact ccggctacgt ttgctgtccc aacaaataga 60
ccagggttcc ctaagtgtcg cttcctccaa gaagccctcc ctgatgagtt gagccacttt 120
agtttgtgct caggctcacc ctgcacgtct tggttgctct catcactgta atgatctaaa 180
acacacgtct gctcatgaga cccgcatccc acccccgatg ctggggccgc tcttggattt 240
tcatgcctgc tgccagcacc caggggggagc tccggaaatg tctgctgggg gctcggaata 300
cccacctttc tggtaatgca gcccagcggg tcccagcctc gttntccagc cctcactcan 360
aatggagtcg ctctggttcg aacgcctctg acaagtgtgt acctacgtgt 410

<210> 236
<211> 394
<212> DNA
<213> Homo sapiens

<400> 236
ggcacgagac tccggctacg tttgctgtcc caacaaatag accagggttc cctaagtgtc 60
gcttcctcca agaagccctc cctgatgagt tgagccactt tagtttgtgc tcaggctcac 120
cctgcacgtc ttggttgctc tcatcactgt aatgatctaa aacacacgtc tgctcatgag 180
acccgcatcc cacccccgat gctggggccg ctcttggatt ttcatgcctg ctgccagcac 240
ccaggggggag ctccggaaat gtctgctggg ggctcggaat acccaccttt ctggtaatgc 300
agcccagcgg gtcccagcct cgttttccag ccctcactca aaatggagtc gctctggttc 360
gaacgcctct gacaagtgtg tacctacgtg tcag 394

<210> 237
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(428)
<223> n = A,T,C or G

<400> 237
ttcggcacga nnnaagaaga ggccctcaga gatctgacag cctatgagtg cgtggacacc 60
acctcagccc actgagcagg agtcacagca cgaagaccaa gcgcaaagcg acccctgccc 120
tccatcctga ctgctcctcc taagagagat ggcaccggcc agagcaggat tctgccccct 180
tctgctgctt ctgctgctgg ggctgtgggt ggcagagatc ccagtcagtg ccaagcccaa 240
gggcatgacc tcatcacagt ggtttaaaat tcagcacatg cagcccagcc ctcaagcatg 300
caactcagcc atgaaaaaca ttaacaagca cacaaaacgg tgcaaagacc tcaacacctt 360
cctgcacgag cctttctcca gtgtggccgc cacctgccag acccccaaaa tagcctgcaa 420
gaatggcc 428

<210> 238
<211> 432
<212> DNA

<213> Homo sapiens

<400> 238
tctcatggag gaacccatcc attcgaattc ggcacgagga tcaactggct atcatatctg 60
tttaatacat ttactggagc cagaaaccta ggccatcatc gaacgccagc ccttggtctg 120
agcctgcggc tgtagatgtg gaactcacag catatgcatt gttggcccag cttaccaagc 180
ccagcctgac tcacaaggag atagcgaagg ccactagcat ataggcttgg ttggccaagc 240
aacgcaatgc atatgggggc ttctcttcta ctcacgatac tgtagttgct gtacaagctc 300
ttgccaaata tgccactacc gcctacgtgc catctgagga gatcaacctg gttgtaaaat 360
ccactgagaa tttccagcgc acattcaaca tacagccagc taacagattg gtatttcagc 420
aggataccct gc 432

<210> 239
<211> 373
<212> DNA
<213> Homo sapiens

<400> 239
ggcacgaggc aggacctcct ctcccagatc gcccagctgc aggaggagaa caagcagctc 60
atgaccaacc tctcccacaa ggatgtcaac ttctcagagg aggagttcca gaagcatgaa 120
ggcatgtcag agcgggagcg acaggtgatg aacaagctga aggaggtggt ggacaaacaa 180
cgcgacgaga tccgcgccaa ggacagggag ctgggcctga aaaatgagga cgttgaggct 240
ttacagcagc agcagacacg gctgatgaag atcaaccatg accttcggca ccgggtcacg 300
gtggtggagg cccaggggaa agccctgatc gaacagaagg tggagctgga ggcagacctg 360
cagaccaagg agc 373

<210> 240
<211> 392
<212> DNA
<213> Homo sapiens

<400> 240
ggcacgagag ctgaccgaga tggacgtttt ctacatcgcg tcgcttgtgg gccacgagtt 60
cgagcgggtc attgaccagc acgggtgtta ggccatcgcg cgcctcatgc ccaaggtcgt 120
gcgcgtgctg gagatcttgg aggtgctggt cagtcgcctc cacgtcgcgc ccgagctgga 180
cgatctgcgc ctggagcagg acctcctctc ccagatcgcc cagctgctgg aggagaacaa 240
gcagctcatg accaacctct cccacaagga tgtcaacttc tcagaggagg agttccagaa 300
gcatgaaggc atgtcagagc gggagcgaca ggtgatgaag aagctgaagg aggtggtgga 360
caaacaacgc gacgagatcc gcgccaagga cg 392

<210> 241
<211> 434
<212> DNA
<213> Homo sapiens

<400> 241
gatcccatcc attcgaattc ggcacgagga ttgattcacc ttcacctgtg ctgcactcca 60
gctgacccaa gtaggaagcc ggacgagctg taaaacatga acggaagagt ggattatttg 120
gtcactgagg aagagatcaa tcttaccaga gggccctcag ggctgggctt caacatcgtc 180
ggtgggacag atcagcagta tgtctccaac gacagtggca tctacgtcag ccgcatcaaa 240
gaaaatgggg ctgcggccct ggatgggcgg ctccaggagg gtgataagat cctttcggta 300
aatggccaag acctaaagaa cctgctgcac caggatgctg tagacctctt tcgtaatgca 360
ggctatgctg tgtctctgag agtgcagcac aggttacagg tgcagaatgg acctatagga 420
catcgaggtg aagg 434

<210> 242
<211> 385
<212> DNA
<213> Homo sapiens

<400> 242
ggcacgagga gagcgcggac acctcctcaa cccactgaac aggagtcaca gcacgatgac 60
cattcgcaaa gcgacccctg ccctccatcc tgactgctcc tcctaagaga gatggcaccg 120

gccaaaacag gattatgccc ccttctgctg cttctgctgc tgccgctgag tgtggcagag 180
atcccactca gtgccaaacc caagggcatg acctcatcac agtggtttag aattcagcac 240
atgcagccca gccctcaagc atgcaactca gccatgaaaa acattaacaa gcacacaaaa 300
cggtgcaaag acctcaacac cttcctgcac gagcctttct ccagtgtggc cgccacctgc 360
cagaccccca aaatagcctg caaga 385

<210> 243
<211> 388
<212> DNA
<213> Homo sapiens

<400> 243
ggcacgagag aaggcctgcg gcaaagagat gagcttattg acaaacatgg cttagttata 60
atcccccgatg gcactcccaa tggtgatgtc agtcatgaac cagtggctgg agccatcact 120
ggtgcgtctc aggaagctgc tcaggtcttg gagtcaccag gagaagggcc attacatgtt 180
tggctacgaa aacttgctgg agagaaggaa gaactactgt cacagattac aaaactgaag 240
cttcagttag aggaggaacg acagaaatgc tccatgactg atggcacagt gggtgacctg 300
gcaggactgc agaatggctc agacttgcag gtcatcgaaa tgcagagaga tgccaataga 360
caaattagcg aatacaaatt taagcttg 388

<210> 244
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(388)
<223> n = A,T,C or G

<400> 244
ggcacgaggt cactgttgaa gagttcaatc ttaccagagg gccctcaggg ctgggcttca 60
acatcgccgg tgggacagat taccagtatg tctccaacga cagtggcatc tacgtcagcc 120
gcatcaaaga aaatggggct gcggccctgg atgggcggct ccaggagggg gataagatcc 180
tttcggtaaa tggccaagac ctaaagaacc tgctgcacca ggatgctgaa cacctctttc 240
gtaatgcagg ctatgctgtg tctctgagag tgcagcacag gttacaggcg cagaatgtac 300
ctataggaca tcgaggtgaa ggggacccaa gcggattccc atatttattg tgctggtgcc 360
cgnggctggc ctctccctgg tattcgcg 388

<210> 245
<211> 390
<212> DNA
<213> Homo sapiens

<400> 245
ggcacgaggc tgtgtgtctc ttttctcacc ccagggcctg gccatgtccc ctttgggaag 60
cctgttccct tacccctaca cgtacatggc cgcagcggcg gccgcctcct ctgcggcagc 120
ctccagctcg gtgcaccgcc acccccttcct caatctgaac accatgcgcc cgcggctgcg 180
ctacagcccc tactccatcc cggtgccggt cccggacggc agcagtctgc tcaccaccgc 240
cctgccctcc atggcggcgg ccgcggggcc cctggacggc aaagtcgccg ccctggccgc 300
cagcccggcc tcggtggcag aggactcggg ctctgaactc aacagacgct cctccacgct 360
ctcctccagc tccatgtcct tgtcgcccag 390

<210> 246
<211> 397
<212> DNA
<213> Homo sapiens

<400> 246
ggcacgagac cactgggacc tcctgctcct cgccatcatc aacacagggc tgtctctgtt 60
tgggctgcct tggatccatg ccgcctaccc ccactccccg ctgcacgtgc gagccctggc 120
cttagtggag gagcgtgtgg agaacggaca catctatgac acgattgtga acgtgaagga 180
gacgcggctg acctcgctgg gcgccagcgt cctggtgggc ctgtccctgt tgctgctgcc 240

ggtcccgctt cagtggatcc ccaagcccgt gctctatggc ctcttcctct acatcgcgct 300
cacctccctc gatggcaacc agctcgtcca gcgcgtggcc ctggtggttc aggaaccaaa 360
ctggggaacc ccccgacaca ctacatcccg gaggggg 397

<210> 247
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

<400> 247
ttacggcgcg tttgttaggg gaccccaccg attcgaattc ggcacgagct ctttttattt 60
tcgctgatat ctttctttta ctaaatgcca ccatccttac ctgttcgggt gtctgcgtgc 120
ctaatttttc ctggctgtta cacaagaacc cggattttag ttgaactctg gagcaaaaat 180
cctgcatcat ttgtaggtgg gtgtcattgt gactggctgc tacctcccca tgagtcttct 240
aaaataaaac ctgcaaattc acatcttccc catgcttcca gagaatgcat attcttcctt 300
tgaaaaaaga aaacnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnggat g 471

<210> 248
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

<400> 248
ggcacgaggt acagacatct agttggcagg agccaaagat gttgccaaac atgtagtann 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnga gtagaggatg cctggtatga ggcaatattt gggataggga agggaagctt 180
gggattttag ctacgtagag acacttgaaa attggaggga ggaaaggagt gggtggcttt 240
ggagatgttc tggaatatgt gaatgagggg agtggagggg ncctgnnngc tctgnggaag 300
gccangcccg gtttcctgtc tttcancctc ttccaggaaa attacgggca gaaagaggct 360
gagaaagtgg tcccggggaa ggcgctttat gaagagcttg gtg 403

<210> 249
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(316)
<223> n = A,T,C or G

<400> 249
ccgcttaaag gcgccttctt ttaatgcaat cattttgaac atgtgcgaca gtcgagaata 60
ctaattggat caatcttgat atactctacc taaagacagt ctagaaacct gggggagaaa 120
gaactcacgg cacaaaacat tgggccgaga acggaattct ctgtaagcct agttgctgaa 180
acttcctgct gtaaccagaa gccagtttta tctatcggct actgaaacac ccactgtgtg 240
ttgctcactc cctcactcac cgaacanaac ctgctacctc cgcatgaatc tactagtgcc 300
gataaactat atcaga 316

<210> 250
<211> 419

<212> DNA
<213> Homo sapiens

<400> 250
ggcacgagat atcagtcaag ggctcttcaa gacacagcag aaacctcacc gggcctcggg 60
ctgcctccca ctgggtccca tggccaccac cttgaccttg gaaagctctg ttatatggaa 120
ggtagggagg acactatttc cctcaactac ttctagtaaa aagctcagtt ctctccccag 180
cagcaagagg gcacctgtga acacctgagt cacagcgcat tcctcctctg cttagaacat 240
tcgatggctc ccaccttact tgcagtaaat gctgaggtcc ttcctgtggc ccccggggcc 300
ctgcatgatc tgatccatcc cttacctacc ctcatctctc cactggcctc cccacacttg 360
ctcccctccg gacactctgg actacttgct gctatctgaa cataccaggc ccctgcccc 419

<210> 251
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(434)
<223> n = A,T,C or G

<400> 251
ggcacgaggg ggcctccacc ggtgactcgg gcctggattc cacggccatg gcctctgccg 60
ctgcggcgca gggactgtcc ggggcgtccg cggacaccct gcccttccac ctccagcagc 120
acgtcctggc ctctcagggc ctggccatgt ccccttcgg aagcctgttc ccttacccct 180
acacgtacat ggacgcagcg gcggccgcct cctctgcggc agcctccagc tcggtgcacc 240
gccacccctt cctcaatctg aacaccatgc gcccgcggct gcgctacagc ccctactcca 300
tcccggtgcc ggtcccggac ggcagcagac tgctcaccac cgccctgccc tccatggcgg 360
cggccgcggn gcccctggac ggcaaagacg ccgccctggc cgccagcccg gcctcggagg 420
cagtggactc ggcg 434

<210> 252
<211> 425
<212> DNA
<213> Homo sapiens

<400> 252
ggcacgagaa agcactcagc ctggggaatg aactctgcca caatgatgat ggctgtgacc 60
actccccgca gagagttctt gaagaggagc tcggcaggga ctggcaggcc aaggtggcct 120
ccttggagga ggtgcccttt gccgctgcct caattgggca ggtgcaccag ggcctgctga 180
gggacgggac ggaggtggcc gtgaagatcc aggtgagagg ggaggctggg cagggtaggg 240
gcgggcaccc tgctagccca gagaagtgac tcccaccttc tctccctccc ttctcccttt 300
acagtacccc ggcatagccc agagcattca gagcgatgtc cagaacctgc tggcggtact 360
caagatgagc gcggccctgc ccgcgggcct gtttgccgag cagagcctgc aggccttgca 420
gcagg 425

<210> 253
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 253
ggcacgagca gacatctagt tggcaggagc caaagatgtt gccaaacatg tagtannnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnngagta gaggatgcct ggtatgaggc aatatttggg atagggaagg gaagcttggg 180
attttagcta cgtagagaca cttgaaaatt ggagggagga aaggagtggg tggctttgga 240
gatgttctgg aatatgtgaa tgaggggagt ggaggggtcc tggaggctct ggggaaggcc 300

```
aagcccgttt tcctgtcttt caacctcttc caggaaaatt acgggcagaa ggaggctgag     360
aaagtggccc gggtgaatgc gctatatgac gagct                                395
```

<210> 254
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(307)
<223> n = A,T,C or G

<400> 254

```
agtcgtcttc ttttaatgta atcattttga acatgtgtga aagttgatca tacgaattgg      60
atcaatcttg aaatactcaa ccaaaagaca gtcgagaagc caggggggaga aagaactcag     120
ggcacaaaat attggtctga gaatggaatt ctctgtaagc ctagttgctg aaatttcctg     180
ctgtaaccag aagccagttt tatctaacgg ctactgaaac acccactgtg ttttgctcac     240
tccctcactc accgatcaaa acctgctacc tccccaagac tttactagtg ccgataaact     300
ttctcan                                                               307
```

<210> 255
<211> 312
<212> DNA
<213> Homo sapiens

<400> 255

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agtcgtcttc ttttaatgta atcattttga acatgtgtga aagttgatca tacgaattgg      60
atcaatcttg aaatactcaa ccaaaagaca gtcgagaagc caggggggaga aagaactcag     120
ggcacaaaat attggtctga gaatggaatt ctctgtaagc ctagttgctg aaatttcctg     180
ctgtaaccag aagccagttt tatctaacgg ctactgaaac acccactgtg ttttgctcac     240
tccctcactc accgatcaaa acctgctacc tccccaagac tttactagtg ccgataaact     300
ttctcaaaga gc                                                         312
```

<210> 256
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(415)
<223> n = A,T,C or G

<400> 256

```
ggcacgagca ggagcagctg gcaagggaga aggacacggt gaagatgctg caggaacagc      60
tggaaaaggc agcgcgtgcc tggcgccaaa gcagggcggg aggagtcgag ctgccgggag     120
ccccggggag gcaggaccgg gagaggcaga gctgggcgga gtcgtcaagc tgctgggagc     180
gctgggctgg gagccccagg ggaggcagag ctgggcggag gtagtgggga cagagacttc     240
ctaacgaggg cttcagccca cccggcccac cacccaccct tctggggttc ccttgctggg     300
aagcgagtgt ctgatccccc tgctggccca ggtcctcact ttgcacctgt gtgggcccct     360
tagccagtgc tccagcccct gccctgcagg atgatggttt cccctcagct cccan          415
```

<210> 257
<211> 396
<212> DNA
<213> Homo sapiens

<400> 257

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agaaagggtg agtgaggtgc tgtcctgggg ttctccaagt ttgagagcat ggatgcatgt      60
ggtttgaagc tgaagtgggc ctgggggaat gggttgaagg cagaagcaac cagtttggag     120
ggaaggcatt tggatatcca gccctttctc tgtggccttg gccctgggtc tgtcctgtta     180
cccccaccca tacctgtctg ctgcgcactc tgtgcttctg tagcattctc gcttctggcc     240
```

tttaaagttg gcaaggggag gttaataagc acctaggtgg ctgagtgtct ctgtcttctg 300
gcttgttcac aggacttcga gtaagaaggt gatttacagc cagcctagtg cccgaagtga 360
aggagaattc aaacagacct cgtcattcct ggtgtg 396

<210> 258
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 258
gnnggagggc ctgcggcaaa gagatgagct tattgagaaa catggcttag ttataatccc 60
cgatggcact cccaatggtg atgtcagtca tgaaccagtg gctggagcca tcactgttgt 120
gtctcaggaa gctgctcagg tcttggagtc agcaggagaa gggccattag atgtaaggct 180
acgaaaactt gctggagaga aggaagaact actgtcacag attagaaaac tgaagcttca 240
gttagaggag gaacgacaga aatgctccag gaatgatggc acagtgggtg acctggcagg 300
actgcagaat ggctcagact tgcagttcat cgaaatgcag agagatgcca atagacaaat 360
tagcgaatac aaatttaagc tttcaaaagc agaacaggat ataactacct tggagcaaag 420
tattagccgg c 431

<210> 259
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

<400> 259
ggcacgagca ggagcagctg gcaagggaga aggacacggt gaagaagctg caggaacagc 60
tggaaaaggc agcgcgtgcc tggcgccaaa gcagggcggg aggagtcgag ctgccgggag 120
ccccggggag gcaggaccgg gagaggcaga gctgggcgga gtcgtcaagc tgctgggagc 180
gctgggctgg gagcccccagg ggaggcagag ctgggcggag gtagtgggga cagagacttc 240
ctaacgaggg cttcagccca cccggcccac cacccaccct tctggggttc ccttgctggg 300
aagcgagtgt ctgatccccc tgctggccca ggtcctcact ttgcacctgt gtgggcccct 360
tagccagtgc tccagcccct gccctgcagg atgatggttt cccn 404

<210> 260
<211> 402
<212> DNA
<213> Homo sapiens

<400> 260
ggcacgagat ctccctgcct tgtgagcagc tggccggcgg ctctgggaca ggcggggatg 60
ggagggagtc taccgggcca ctgtagagct ggtagctggg agctggagct gtagagttcc 120
aggctgggag ctggagagcc ctgggtgaga gggaggccta taggggcccc gggggacaca 180
ccaggcttga gggtagtagg tgctggaggc agagcctggc ctgtccaggg tgggacctca 240
cgacccaccc tgtccggccc ccagctcgga ggagcttcta cgtgtatgcg ggcatcctgg 300
cactgctcaa cctactgcag gggctgggga gtgagctgct gtgcttcgac atcatcgagg 360
ggctctggtg cgtgggggcc gcagggagtc tgcctcgtgg gg 402

<210> 261
<211> 402
<212> DNA
<213> Homo sapiens

<400> 261

ggcacgagat ctccctgcct tgtgagcagc tggccggcgg ctctgggaca ggcggggatg 60
ggagggagtc taccgggcca ctgtagagct ggtagctggg agctggagct gtagagttcc 120
aggctgggag ctggagagcc ctgggtgaga gggaggccta gaggggcccc gggggacaca 180
ccaggcttga gggtagtagg tgctggaggc agagcctggc ctgtccaggg tgggacctca 240
cgacccaccc tgtccggccc ccagctcgga ggagcttcta cgtgtatgcg ggcatcctgg 300
cactgctcaa cctactgcag gggctgggga gtgtgctgct gtgcttcgac atcatcgagg 360
ggctctggtg cgtgggggcc gcagggtgtc tgcctcgtgg gg 402

<210> 262
<211> 151
<212> DNA
<213> Homo sapiens

<400> 262
gccgaatatg aagctacgtc cgggtatccg ggttccctgt aattgctttc tgatccctgg 60
tacttagatt tgattaccta tggaccacat tggtagaact actatatggg ggaacctcct 120
gattttgggc ggtctcaaaa acaaaaaaaa c 151

<210> 263
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

<400> 263
ggcacgaggg aacgtggaag gactagactg cctgagtctt ctgannnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnntt 120
ggacctaccc cccgagtggt ttgccagggg ctctcaggcc ttcggctaca gactgagggc 180
tgcattatca gctttcctac ttttgaggtt ttgggacttt actggctttc ttgctcctca 240
acttgcagat ggcctgttgt gggacctcac cttgtgatca tgtacatgag ggaaatacac 300
acccctccca gggatgatgg aaggttaagg tcctaacacc tcctgcacat ctgagcagct 360
gcacattgaa ccagatagtc ctggaatgtg ggaaaacaga ggcn 404

<210> 264
<211> 380
<212> DNA
<213> Homo sapiens

<400> 264
ggcacgaggg gaacgggaag ccgggaccca gaactcttgt ctttcaggat aaagtggcca 60
gggtgtacga agccccgggc tttttcctgg acctggagcc catcccggga gccttggacg 120
ctgtgcggga gatgaacgac ctaccggaca cgcaggtctt catctgcacc agccccctgc 180
tgaagtacca ccactgtgtg ggtgagaagt accgctgggt ggagcagcac ctggggcccc 240
agttcgtaga acgaattatc ctgacaaggg acaagacggt ggtcttgggg gacctgctca 300
ttgatgacaa ggacacagct cgaggccagg aggagacccc aagctgggag cacatcttgt 360
tcacctgctg ccacaatcgg 380

<210> 265
<211> 440
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(440)
<223> n = A,T,C or G

<400> 265
ggcagaggcg tggacaccac ctcagcccac tgagcaggag tcacagcacg aagaccaagc 60

gcaaagcgac ccctgccctc catcctgact gctcctccta agagagatgg caccggccag 120
agcaggattc tgccccctc tgctgcttct gctgctgggg ctgtgggtgg cagagatccc 180
agtcagtgcc aagcccaagg gcatgacctc atcacagtgg tttaaaattc agcacatgca 240
gcccagccct caagcatgca actcagccat gaaaaacatt aacaagcaca caaaacggtg 300
caaagacctc aacaccttcc tgcacgagcc tttctccagt gtggccgcca cctgccagac 360
ccccaaaata gcctgcaaga atggcgataa aaactgccac caaagccacg ggcccgtgtt 420
cctgaccatg tgaagctccn 440

<210> 266
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 266
gcacgaggag gaacgtggaa ggactagact gcctgagtct tctgannnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnt 120
tggacctacc ccccgagtgg tttgccaggg gctctcaggc cttcggctac agactgaggg 180
ctgcattatc agctttccta cttttgaggt tttgggactt tactggcttt cttgctcctc 240
aacttgcaga tggcctgttg tgggacctca ccttgtgatc atgtacatga gggaaataca 300
cacccctccc agggatgatg gaagggtaag gtcctaacac ctcctgcaca tctgagcagc 360
tgcacattga accagatagt cctggaatgt gggaac 396

<210> 267
<211> 429
<212> DNA
<213> Homo sapiens

<400> 267
ggcacgagga tctgacagcc taggagtgcg tggacaccac ctcagcccac tgagcaggag 60
tcacagcacg aagaccaagc gcaaagcgac ccctgccctc catcctgact gctcctccta 120
agagagatgg caccggccag agcaggattc tgccccctc tgctgcttct gctgctgggg 180
ctgtgggtgg cagagatccc agtcagtgcc aagcccaagg gcatgacctc atcacagtgg 240
tttaaaattc agcacatgca gcccagccct caagcatgca actcagccat gaaaaacatt 300
aacaagcaca caaaacggtg caaagacctc aacaccttcc tgcacgagcc tttctccagt 360
gtggccgcca cctgccagac ccccaaaata gcctgcaaga atggcgataa aaactgccac 420
cagagccac 429

<210> 268
<211> 405
<212> DNA
<213> Homo sapiens

<400> 268
ggcacgaggc ggcttcctgg cccgcgagca gtaccgcgcc ctgcggcccg acctggcgga 60
taaagtggcc agtgtgtacg aagccccggg ctttttcctg gacctggagc ccatcccggg 120
agccttggac gctgtgcggg agatgaacga cctaccggac acgcaggtct tcatctgcac 180
cagcccctg ctgaagtacc accactgtgt gggtgagaag taccgctggg tggagcagca 240
cctggggccc cagttcgtag aacgaattat cctgacaagg gacaagacgg tggtcttggg 300
ggacctgctc attgatgaca aggacacagt tcgaggccag gaggagaccc caagctggga 360
gcacatcttg ttcacctgct gccacaatcg gcacctggcc tgccc 405

<210> 269
<211> 372
<212> DNA
<213> Homo sapiens

<400> 269
ggcacgagaa ccctgaggcc tggctatggt accaccgggt ggtaggtgcc cagcgctgcc 60

ccatcgtgga caccttctgg caaacagaga caggtggcca catgttgact ccccttcctg 120
gtgccacacc catgaaaccc ggttctgcta ctttcccatt ctttggtgta gctcctgcaa 180
tcctgaatga gtccggggaa gagttggaag gcgaagctga aggttatctg gctgccagcg 240
ggaccaggat ggctattact ggatcactgg caggattgat gacatgctca atgtatctgg 300
acacctgctg agtacagcag aggtggagtc agcacttgtg gaacatgagg ctgttgcata 360
ggcacctgtg gg 372

<210> 270
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(411)
<223> n = A,T,C or G

<400> 270
ggcacgagag ctctcggcgc acggcccagc ttccttcaaa atgtctactg ttcacgaaat 60
cctgtgcaag ctcagcttgg agggtgattg tccaggaagt tattccagat gaagacttat 120
acnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 240
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn n 411

<210> 271
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(302)
<223> n = A,T,C or G

<400> 271
ctgagtgtga cactcagaga gtgtgttata tagacagaga gagagcgcgc gcctctgtcc 60
ccccccttgt gtgtgcccca ctccagtgcg cccagatccg tgcccccccc cggagcgccg 120
tgctccctnn nnnnnnnnag tgtgcacacc cccctccccc tctcatgagt gcccacatat 180
atattcctgt gtgacccctc cccccccctg ccagtcagtg tccccgccgg agcgcgagtc 240
actgttttat tttttctcgc ccccaagaag ggatagcgat gtgtctctcc cctcctccca 300
ca 302

<210> 272
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(429)
<223> n = A,T,C or G

<400> 272
ggcacgagat gtggtacaga catctagttg gcaggagcca aagatgttgc caaacatgta 60
gtannnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnngagtaga ggatgcctgg tatgaggcaa tatttgggat agggaaggga 180
agcttgggat tttagctacg tagagacact tgaaaattgg agggaggaaa ggagtgggtg 240
gctttggaga tgttctggaa tatgtgaatg aggggaagtg gaggggcctg gaggctctgg 300
ggaaggccaa gcccgttttc ctgtctttca acctcttcca ggaaaattac gggcagaagg 360
aggctgagaa agtggcccgg gtgaaggcgc tatatgagga gctggaactg tcaacagtgg 420
tcttgcaaa 429

<210> 273
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(471)
<223> n = A,T,C or G

<400> 273
tgttgtgcat ttgggcatcc caccgattcg aattcggcac gagaaagcat tgaagagacc 60
tcaaggcttt aagaaatgag taggccaaaa tctaagtcaa aggagaatct gtactggggc 120
cccccgtgcc ctgaggtcat tggccaagcc aagccgaacc tgagctttga tcctgatggt 180
ttggggagtg aggaagacag aagtggaagc ccagttctca ccccaagagg ggacacaaat 240
ggatgaccct cccatgatgc tgagacccca aaaggctaca cactcaagct aaaagccaga 300
ggaaatccca tcctgccacc cacaagactt caaggaaagt tgttttggtg ctgagcagag 360
caggggaaga aggaaaacag cccttaagga gctccagcca ctggccagcc ttcatgtgac 420
tctagcccaa attcattccc atcacctggg gtggaagggc cagaaatctc n 471

<210> 274
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 274
ggcacgaggt aaactctcta taagtgttca gtgttgacat agcctttgtg catagnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnttt tttgccccac ctggaaaaaa ggggatgcnn 120
nnnnnnnngg ggggaaaaac aattcttaag ggccctttgg ccataaactt ttttccgggc 180
cacctttgtt acttttggtc ctggaagggg tttttttggg gggcccacgg ggaggggccc 240
cataggtaaa ctcggaaaac tttttctaac ccgggttagt gttttaaatt aaaaccaaaa 300
annnnnnnnn nnttggaatc cttttcttta aaaaaattaa tctctcaaag gaaaacaaag 360
nnnnnnnnnn ngggggggccc ctttcgttta g 391

<210> 275
<211> 339
<212> DNA
<213> Homo sapiens

<400> 275
cactccgggg gctctatttg tgtgctctgc acccagtttt ttatacactc cacgctttgg 60
atataacatc tagcgccacg gtgcctatgt gtacacaccc tctctctata tatagatacc 120
tctgtgcgca catatagagg ggaaaagaga gatatatcta ttatatatac atttctacac 180
aactgtctct gggggggtcag agaacgcgcg cacccctctc ttttgagaga aggagactct 240
gtccccccctc tctggggcgc agggaggccc catggcatga agaaaaatac tcacttatat 300
ctctctctct cactctctgt ttgcgaaaaa acacacagg 339

<210> 276
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(434)
<223> n = A,T,C or G

<400> 276

```
ccctagctac ttgctctttg tgcaggatgc catagattcg tgggctcctg ccttttctca      60
accccgaggt gcctgaccag ttctaccgcc tgtggctatc cctcttcctg cacgccggga     120
tcttgcactg cctggtgtcc atctgcttcc agatgactgt cctgcgggac ctggagaagc     180
tggcaggctg gcaccgcata gccatcatct acctgctgag tggtgtcacc ggcaacctgg     240
ccagtgccat cttcctgcca taccgagcag aggtgggtcc tgctggctcc cagttcggca     300
tcctggcctg cctcttcgtg gagctcttcc agagctggca gatcctggcg cggccctggc     360
gtgccttctt caagctgctg gctggggagg cttttctctt cacctttggg ctgctgccgt     420
ggattgacaa cttn                                                       434
```

<210> 277
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(378)
<223> n = A,T,C or G

<400> 277

```
ggcacgagaa aaagtaccgc tccagagcag gagcctaggc agccgagagg gtgcccgaac      60
ctgagtctga gttgcggcca cttcaggagc tgagaggagc aggatggaac tgcaggatcc     120
aaagatgaat ggagccctcc cttcggatgc tgtgggctac aggcaagaac gtgagggctt     180
cctgcccagt cgtggtcctg ctcctgggag caagccggtc cagttcatgg atttcgaggg     240
gaagacatcg tttggaatgt cagtgttcaa cctcagcaac gccatcatgg gcagcggcat     300
cctggggctg gcctatgcca tgggccacac gggggtcatt ttctttctgg gcctgctgct     360
gngccatgcg cttctgcc                                                   378
```

<210> 278
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(302)
<223> n = A,T,C or G

<400> 278

```
cccccnctct cgccnnnnnn nnnnncgttt tcactcccgg gagtcccctt gtttttggcc      60
cggatccggg ttctttcttt cccgtggtgc cgcgggttgg agtgttttat cttttcttca     120
catgggggc tggggagttc cccagaaccc ccagggggaa acccccctcc tatgaaaatg      180
acacatgagc ccctccttcc ggtggcgggg acctgtctct ctaagaccct tttctgggaa     240
aggggtcttt gtttgtatga ccccaccgac gcgggggct ttctatgggc cgcccccccc      300
cg                                                                    302
```

<210> 279
<211> 405
<212> DNA
<213> Homo sapiens

<400> 279

```
ggcacgaggc ctcattggag acattgacaa tgccatgagg accttcctca actactacac      60
tgtatggaag cagtttgggg ggctcccgga attctacaac attcctcagg gatacacagc     120
ggagaagcga gagggctacc cacttcggcc agaacttatt gaaagcgcaa tgtacctcta     180
ccgtgccacg ggggatccca ccctcctaga actcggaaga gatgctgtgg aatccattga     240
aaaaatcacc aaggtggagt gcggatttgc aacaatcaaa gatctgcgag accacacgct     300
ggacaaccgc atggagtcgt tcttcctggc cgagactgtg aaatacctct acctcctgtt     360
tgacccaacc aacttcatcc acaacaatgg gtgcaccttc gacgc                     405
```

<210> 280
<211> 415
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(415)
<223> n = A,T,C or G

<400> 280
ggcacgaggg tcacctgtgc tgcccctcct taatctcgta tgatggtcac agtccggtgg 60
ccgtgggggt gctctgcctt ccctggtccc cactgcccat atctgtggac tgccccttcc 120
aaagacccct gggggggtt gganaanattc aatcttacca aactcaacga tccatccatt 180
tcatgttact gatattacat gcggacaccc ctggatcata ttattcaaat ccagtcatct 240
attctgcatt catgaccttt tgataactcc atcatgacct acttgacggt cactgaccat 300
gcttactgga ttccgccttg taacaataaa atctatttaa actnnnnnnn nnnnnnnnnn 360
nnnaccagcc cacataaaat atgattgaat caatttctta taccttcact agaat 415

<210> 281
<211> 389
<212> DNA
<213> Homo sapiens

<400> 281
ggcacgaggt agactggggg ctcactgatt gcattgacac ttttcatcat gggtccccgg 60
gggctcacgt ggagtctgac acatgaatac atggctatca tgtctgtcac cttcaatggg 120
gaaaacaaac tttgtaatgg taggaaacac aacaggtaca ataatttaca aaaatatgtt 180
tgccacattt cagggcaagg caaaatgcag aggagacata tgttaaaatc ttatcattca 240
catttgttct ttttatcttt aagatgaagc tcttacacca agtgtcacga gtctggagaa 300
cagatgggtt gaagagctgt tcttataaaa taagatctgg ggaacacaat cctttatata 360
tcaacatcac agtggatttt tggattggg 389

<210> 282
<211> 371
<212> DNA
<213> Homo sapiens

<400> 282
ggcacgagat agaatccgag gcattgatat cattaaatgg atggagcgct accttaggga 60
taagaccgtg atgataatcg tagcaatcag ccccaaatac aaacaggacg tggaaggcgc 120
tgagtcgcag ctggacgagg atgagcatgg cttacatact aagtacattc atcgaatgat 180
gcagattgag ttcataaaac aaggaagcat gaatttcaga ttcatccctg tgctcttccc 240
aaatgctaag aaggagcatg tgcccacctg gcttcagaac actcatgtct acagctggcc 300
caagaataaa aaaaacatcc tgctgcggct gctgagagag gaagagtatg tggctcctcc 360
acgggggcct c 371

<210> 283
<211> 413
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

<400> 283
ggcacgaggt gggagacacc acttgtcttt atgtgggtct caaagatgat gtagaatttc 60
ctttaatttc tcgcagtctt cctggaaaat attttccttt gagcagcaaa tcttgtaggg 120
atatcagtga aggtctctcc ctccctcctc tcctgnnnnn nnnnnnngga aacaaagttt 180
tgcttttgtt ccccagcctg aaggggaagg gctcaatttt ggttaaccaa aaccttggcc 240
tccggggtta aagcaattct ccggcctaac cctttggaga acctgggtta ataggcgcag 300
gcccccaggc cgggttaatt ttgggtttta agaaaaaaca gggtttctca atgtggggca 360
ggcgtggcca aaaccccсac cctaagggga tcggccctcc ttggcctccc aan 413

<210> 284
<211> 409
<212> DNA
<213> Homo sapiens

<400> 284
ggcacgaggc ctggggatgc tccctgctaa gtgggcctgc tcccaccctt gccataaagc 60
tctgaggcag cctgagcctg ccgtgggggc cccactgtga ccctgccgca gtcttcctgg 120
gtccctgcgt cctcttaagg ggcagtgaca cctgcctcgc tggccctgtg tgggtggcag 180
gccccactgt ttgggatatc acatggccag gcacgtggtg agcctgctca gggcggacgc 240
ctgcaggcgc gtgctcggtc acacactgcc ttgtgtggcc ctcctgtccg gtgcagcctg 300
gacctggacg cctggatcaa tgagccactc tcggacagcg agtcagagga cgagaggccc 360
agggccgtct tccacgagga ggagcagcgg cgtcccaagc accggccgt 409

<210> 285
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(404)
<223> n = A,T,C or G

<400> 285
ggcacgagcc acttcacccc cttgggggct gcttattcac tctggggatt cgccatggac 60
acgtctcaac tgcgcaagct gctgcccatg tttccctgcc cctccagatt gcctggagat 120
ctattttgtt tccttttgtg tttctttttc tgttttgagt gtctttcttt gcaggtttct 180
gtagccggaa gatctccgtt ccgctcccag cggctccagt gtaaattccc cttccccctg 240
gggaaatgca ctaccttgtt ttgggggtt taggggtgtt tttgtttttc agnngntttg 300
ntttttttggn nnnnnnnnnn gntttgactt ttttnncttt tattttggag ggtaatggaa 360
agaataggaa aatcaggcag gggggagaat ggttgtttat tctt 404

<210> 286
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(441)
<223> n = A,T,C or G

<400> 286
ggcacgaggg aagcgggtgg tgtgtgtccc ctgtttactt ttagctgagc tggggttggg 60
tgtacgggtt ctgttcctct gagccctgcg gcccacctga tgtttacgtg tgtgtgtgag 120
ggggggcggc gctncncnnn caccccccan nggcctctat ccttgtgaag ctctcctcaa 180
tctaatactt attgcccctg actccaaatc ttccaccttt tgcctcttat tatatctatg 240
ttcattacct taggtcagct gttctctatt atgacactga ttcatacttt tgttttttga 300
taagtactta tttcctctct cattgttgct aatatcctct tccttttttc ctttgtctac 360
tctcacttca tctataaaac tcttacatat ctctccacta atttctttga actaacaatt 420
tttatataga atttaagcct g 441

<210> 287
<211> 387
<212> DNA
<213> Homo sapiens

<400> 287
ggcacgagca gccctggaat tccgcaagca cccggaggcc gggggtctc cgcgggcgtc 60
ccatgcggag gacatggtgc gccgtgtact cttccccacg acctcaggga ccggtccccc 120
cgccggaact gcttcctacc tggtccggtc ccggcagctg aatctggcca gcccaacctc 180
ccggtcgcta tggcacccac aggcctaaca ttcgcgagtc caccttccgc cgtccgcgag 240

gaaaacctga ttggcgccct cttggcgatc ttcgggcacc tcgtggtcag cattgcactt 300
aacctccaga agtactgcca catccgcctg gcaggctcca aagatccccg ggccttattt 360
aaagaccaaa actggtggct tgggcct 387

<210> 288
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 288
ggcacgaggg aggctggaag cgggtggtgt gtgtcccctg tttactttta gctgagctgg 60
ggttgggtgt acgggttctg ttcctctgag ccctgcggcc cacctgatgt ttacgtgtgt 120
gtgtgagggg gggcggcggn nncannnnnn nnnnnnngan tctttttcca ataacaatat 180
taattaatcc aatctttttt cttcttctct tctttctact ctttttcctc cttttttttt 240
atttactttt actcatcctc ctttcttcat ttactctgtc ttttgtatta ctagcttctt 300
ctctttcgca attttccttt attgttgtca ctcttttggg aataacgtac tcttatgaga 360
agttgtttcc tctttattta catttggttg tcttctcctt tcataattta ttttacgtat 420
gtttgtggag ttttttcttt 439

<210> 289
<211> 170
<212> DNA
<213> Homo sapiens

<400> 289
atgagtggtc ttttaattag gaacaaatct aatggaaagg agagttgact gaagttggcc 60
cacaggattg tgagctgggc agagccttca tgaaggcttg ccaccttggg acgcccaatt 120
taatgggggg gcctgctgta aggcaaaagg ctttttggca aattgctggg 170

<210> 290
<211> 393
<212> DNA
<213> Homo sapiens

<400> 290
ggcacgaggt agactggggg ctcactgagt gcagtgacac ttttcatcat gggtccccgg 60
gttctcacgt ggagtctgac acatgaatac atggctatca tgtctgtcac cttcaatggg 120
gaaaacaaac tttgtaatgg taggaaacac aacaggtaca ataatttaca aaaatatgtt 180
tgccacattt cagggcaagg caaaatgcag tggagacata tgttaaattc ttatcattca 240
catttgatct ttttatcttt aggatgaagc tcttacacca agtgtcacga gtctggagaa 300
cagatggggt gagtagttgt tcttataaat tagtatctgt ggaacacaat cctttatata 360
tcaacatcac agtggatttc tggcttggtg cat 393

<210> 291
<211> 430
<212> DNA
<213> Homo sapiens

<400> 291
ggcacgaggg atagaatccg aggcattgat atcattaaat ggatggagcg ctaccttagg 60
gataagaccg tgatgataat cgtagcaatc agccccaaat acaaacagga cgtggaaggc 120
gctgagtcgc agctggacga ggatgagcat ggcttacata ctaagtacat tcatcgaatg 180
atgcagattg agttcataaa acaaggaagc atgaatttca gattcatccc tgtgctcttc 240
ccaaatgcta agaaggagca tgtgcccacc tggcttcaga acactcatgt ctacagctgg 300
cccaagaata aaaaaaacat cctgctgcgg ctgctgagaa aagaaaaaga tgtggctcct 360
tcacgggggc ctcttgccac ccttcaagtg ggtcccttgt gacacccgtc aatcccagat 420
cactgaggcc 430

<210> 292
<211> 423
<212> DNA
<213> Homo sapiens

<400> 292
atcccatcga ttcgaattcg gcacgaggga agcaagggca cccgccttat ggatggaatt 60
gaggggaagg cacccggggc tcctgcatcg agcttccctc ctatattcaa tgaggaaatg 120
accctgcaga aggctggctg cagatgcccc tgcctcccgg ctttgcctgc ttggagtttg 180
atggacacgt ggtcctgtca gggctacagc aggtctatgg tctttggtaa cggaaagcgc 240
tggtgaaaca gtgagctttc ccgtgggtgc ttttccctga cgccaacaac cagggcaagc 300
tgcctgtcct gctgcttggc cgctcctcag agctgcggcc gggagagttc gtggtcgcca 360
tcggaagccc gttttccctt caaaacacag tcaccaccgg gatcgtgagc accacccagc 420
gag 423

<210> 293
<211> 409
<212> DNA
<213> Homo sapiens

<400> 293
ggcacgaggc taggagtact ggcctagatg gttatagaag tccatgccag gaggtcgtct 60
gcagtcagag ggtggttctg ggctggactc cagccccttc ctgtcggagg ccaatgccga 120
gcggattgtg cagaccttat gtacagttcg aggggccgcc ctcaaggttg gccagatgct 180
cagcatccag gacaacagct tcatcagccc tcagctgcag cgcatctttg agcgggtccg 240
ccagagcgcc gacttcatgc cccgctggca gatgctgaga gttcttgaag aggagctcgg 300
cagggactgg caggccaagg tggcctcctt ggaggaggtg ccctttgccg ctgcctcaat 360
tgggcaggtg caccagggcc tgctgaggga cgggacggat gtgggcgtg 409

<210> 294
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 294
ggcacgaggc cagctgctgg tggagcggca ctggggactg gaggctggaa gcgggtggtg 60
tgtgtcccct gtttactttt agctgagctg gggttgggtg tacgggttct gttcctctga 120
gccctgcggc ccacctgatg tttacgtgtg tgtgtgaggg ggggcggngn nnnnnnnnnn 180
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnna 240
nnnnnnnnnn ntnaatatat ttttttgttt aatgggtnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnataaatt 360
attaaattt 369

<210> 295
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

<400> 295
ggcacgagtg cttctctagc tctctaggcc tctccagttt gcacctgtcc ccaccctcca 60
ctcagctgtc ctgcagcaaa cactccaccc tccaccttcc attttccccc actactgcag 120
cacctccagg cctgttgcta tagagcctac ctgtatgtca ataaacaaca gctgaagcnn 180
nnnnnnnnnn nnnnncccccg ccccttaaaa acaatggggg gccgtttacc gaaaacccaa 240

actggaaaaa acccttggtg gagttggacc acccccccacc taaagggcgg ggaaaaaaag 300
gctttattgg aaaaattggg gaggctttgg tttaattgga acccataaaa gccggcaaaa 360
aacaggtaac caccaccatt ggctttcttt ttaggttcag ggg 403

<210> 296
<211> 384
<212> DNA
<213> Homo sapiens

<400> 296
ggcacgagga gaacttctgg atcgggccca gctcggaggc cctcatccac ctgggcgcca 60
agttttcgcc ctgcatgcgc caggacccgc aggtgcacag cttcattcgc tcggcgcgcg 120
agcgcgagaa gcactccgcc tgctgcgtgc gcaacgacag gtcgggctgc gtgcagacct 180
cggaggagga gtgctcgcta acaggaatta tgccgtcaaa ctcctttcca cgctggcagt 240
gtgggtgaag tggcccatcc atcccagcgc cccagagctt gcgggccaca agagacagtt 300
tggctctgtc tgccaccagg atcccagggt gtgtgatgag ccctcctccg aagaccctca 360
tgagtggcca gaagacatca ccaa 384

<210> 297
<211> 401
<212> DNA
<213> Homo sapiens

<400> 297
ggcacgagat taagtgaatt gcgttatatt tatgacctta aggaccagat acaggaggta 60
gaagggagat acatgcaggg gcttaaagaa ctaaaggaat ctttgtctga agtggaagaa 120
aaatacaaga aagccatggt ttccaatgca cagttagaca atgagaagaa caatttgatc 180
taccatgtag acacactcaa ggatgttatt gaagagcagg aggaacagat ggcagaattt 240
tatagagaaa atgaagaaaa atcaaaggag ttagaaaggc agaaacatat gtgtagtgtg 300
ctgcagcata agatggaaga acttaaagaa ggcctgcggc aaagagatga gcttattgag 360
aaacatggct taagtataat ccccgatggc actcccaatg g 401

<210> 298
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(430)
<223> n = A,T,C or G

<400> 298
aaatgggaga actctgaggt ncccaacgat tcgcattcgg cacgaggcca gctgctgggg 60
gagcggctct ggggactgga ggctggaagc gggtggtgtg tgtcccctgt ttacttttag 120
ctgagctggg gttgggtgta cgggttctgt tcctctgagc cctgcggccc acctgatgtt 180
tacgtgtgtg tgtgaggggg ggcgggnnac gntatanacc catcttatta tcaaattaca 240
aaatcccant aataggtatc tccatcaagc tgcangagga ggagagagaa atgagagaca 300
attatgttcc tgtggtctca gccttggatc aggagattat tgaagatgat tcttgcccta 360
aggagatgct gaagcttttg gactttgggg gtctgttcaa ccttcatggt acttcaactt 420
cagctgggaa 430

<210> 299
<211> 387
<212> DNA
<213> Homo sapiens

<400> 299
ggcacgaggt ttcatacctt ctcagaattg gtatatcaag acacatttaa atataagccc 60
tctggaaatg gatttatata cagtcatcat aattaccccc ttagaaattg gtaatatttt 120
atagccaggt ttaggtttag tgtcaagtat agtgattgct ggtctatcac tactcatgaa 180
gtggaacccc ctctactcat aaaaacccca atcagacata tagatgaata gaaccttgat 240
aacattagaa tgccttgttc tctgaaggct tacaagacta tacgtcagga tatattaagg 300

agaagctgag gaacgaaaga aacttcgaca agagaatgga aatgtacatg ctatagcata 360
actgaagaat aaaatacagg tttgagg 387

<210> 300
<211> 373
<212> DNA
<213> Homo sapiens

<400> 300
ggcacgagac tagtccgact ttttatgtgc tatgcaaaat agacatcttt aacatagtcc 60
tgttactatg gtaacacttt gctttctgaa ttggaaggga aaaaaatgta acgacagcat 120
tttaaggttg ccatggtaac cagccacagt acatatgtaa ttctttccat cacccccaacc 180
tctcctttct gtgcattcat gcaagagttt cttgtaagcc atcagaagtt acttttagga 240
tgggggagag gggcgagaag gggaaaaatg ggaaatagtc tgattttaat gaaatcaaat 300
gtatgtatca tcagttggct acgttttggt tctatgctaa actgtgaaaa atcagatgaa 360
ttgataaaag agt 373

<210> 301
<211> 369
<212> DNA
<213> Homo sapiens

<400> 301
ggcacgagac tagtccgact ttttatgtgc tatgcaaaat agacatcttt aacatagtcc 60
tgttactatg gtaacacttt gctttctgaa ttggaaggga aaaaaatgta gcgacagcat 120
tttaaggttg ccatggtaac cagccacagt acatatgtaa ttctttccat cacccccaacc 180
tctcctttct gtgcattcat gcaagagttt cttgtaagcc atcagaagtt acttttagga 240
tgggggagag gggcgagaag gggaaaaatg ggaaatagtc tgattttaat gaaatcaaat 300
gtatgtatca tcagttggct acgttttggt tctatgctaa actgtgaaaa atcagatgaa 360
ttgataaaa 369

<210> 302
<211> 399
<212> DNA
<213> Homo sapiens

<400> 302
ggcacgaggc agcagacacg gctgatgatg atcaaccatg accttcggca ccgggtcacg 60
gtggtggagg cccaggggaa agccctgatc gaacagaagg tggagctgga ggcagacctg 120
cagaccaagg agcaggagat gggcagcctg cgagcagagc tggggaagtt gcgagagagg 180
ctgcaggggg agcacagcca gaatggggag gaggagcctg agacggagcc ggtgggagag 240
gagagcatct ccgacgcaga gaaggtggcc atggatctca aggaccccaa ccgcccccgg 300
ttcaccctgc aggagctgcg ggacgtgctg cacgagagga acgagctcaa gtccaaggtg 360
ttcttgctgc aggaggagct ggcttactat aagagtgag 399

<210> 303
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

<400> 303
ggcacgagca cagcccctga ctgccgcagc ccccacagag cccgccgcgc accccacgtc 60
ccccacgcca gcgcccagcc atggaggcca tcaagnnnnn nnnnnnnnnn nnnnnnnngg 120
acaaggagaa tgccatcgac cgcgcggagc aggcggaggc ggataagaaa gccgctgagg 180
acaagtgcaa gcaggtggag gaggagctga cgcacctcca gaagaaacta aaagggacag 240
aggacgagct ggataaatat tccgaggacc tgaaggacgc gcaggagaag ctggagctca 300
cggagaagaa ggcctccgac gctgaaggtg atgtggccgc cctcaaccga cgcatccagc 360
tcgttgagga ggagttggac agggctcang a 391

<210> 304
<211> 418
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G

<400> 304
ggcacgagtg ccgcagcccc cacagagccc gccgcgcacc ccacgtcccc cacgccagcg 60
cccagccatg gaggccatca agnnnnnnnn nnnnnnnnnn nnnnnggaca aggagaatgc 120
catcgaccgc gcggagcagg cggaggcgga taagaaagcc gctgaggaca agtgcaagca 180
ggtggaggag gagctgacgc acctccagaa gaaactaaaa gggacagagg acgagctgga 240
taaatattcc gaggacctga aggacgcgca ggagaagctg gagctcacgg agaagaaggc 300
ctccgacgct gaaggtgatg tggccgccct caaccgacgc atccagctcg ttgaggagga 360
gttggacagg gctcangaac gactggccac ggccctgcag aagctggagg aggcagaa 418

<210> 305
<211> 420
<212> DNA
<213> Homo sapiens

<400> 305
ggcacgagga tttcggcaac aatttacaca gctggctgga ccagacatgg aggtgggtgc 60
cactgatctg atgaatattc tcaacaaagt cctttctaag cacaaagatc ttaagactga 120
cggttttagt cttgacacct gccggagcat tgtgtctgtc atggacagtg acacgactgg 180
taagctgggc tttgaagaat ttaagtatct gtggaacaac atcaagaaat ggcagtgtgt 240
ttataagcag tatgacaggg accattctgg gtctctggga agttctcagc tgcggggagc 300
tctgcaggcc gcaggcttcc agctaaatga acaactttac caaatgattg tccgccggta 360
tgctaatgaa gatggagata tggattttaa caatttcatc agctgcttgg tccgcctgga 420

<210> 306
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(399)
<223> n = A,T,C or G

<400> 306
ggcacgagcc acgtccccca cgccagcgcc cagccatgga ggccatcaag nnnnnnnnnn 60
nnnnnnnnnn nnnggacaag gagaatgcca tcgaccgcgc ggagcaggcg gaggcggata 120
agaaagccgc tgaggacaag tgcaagcagg tggaggagga gctgacgcac ctccagaaga 180
aactaaaagg gacagaggac gagctggata aatattccga ggacctgaag gacgcgcagg 240
agaagctgga gctcacggag aagaaggcct ccgacgctga aggtgatgtg gccgccctca 300
accgacgcat ccagctcgtt gaggaggagt tggacagggc tcaggaacga ctggccacgg 360
ccctgcagaa gctggaggag gcagaanaag ctgcagatg 399

<210> 307
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(438)
<223> n = A,T,C or G

<400> 307

atcccatcga ttcgaattcg gcacgagccc ccacagagcc cgccgtgcac cccacgtccc 60
ccacgccagc gcccagccat ggaggccatc aagnnnnnnn nnnnnnnnnn nnnnnnggac 120
aaggagaatg ccatcgaccg cgcggagcag gcggaggcgg ataagaaagc cgctgaggac 180
aagtgcaagc aggtggagga ggagctgacg cacctccaga agaaactaaa agggacagag 240
gacgagctgg ataaatattc cgaggacctg aaggacgcgc aggagaagct ggagctcacg 300
gagaagaagg cctccgacgc tgaaggtgat gtggccgccc tcaaccgacg catccagctc 360
gttgaggagg agttggacag ggctcatgaa cgactgggca cggacctgca gaagctggag 420
gagggcagaa aaagctgc 438

<210> 308
<211> 419
<212> DNA
<213> Homo sapiens

<400> 308
ggcacgagct ttggcctgcc cgctcctctc ctttctggcg acccgactct ggctacgcaa 60
cggggcccgc gtcaatgcct gggcctactg ccacgtgcta cccactgggg acctgctgct 120
ggtgggcacc caacagctgg gggagttcca gtgctggtca ctagaggagg gcttccagca 180
gctggtagcc agctactgcc cacaggtggt ggaggacggc gtggcagacc aaacagatga 240
gggtggcagt gtacccgtca ttatcagcac atcgcgtgtg agtgcaccac ctggtggcaa 300
ggccagctgg ggtgcagaca ggtcctactg gaaggagttc ctggtgatgt gcacgctctt 360
tgtgctggcc gtgctgctcc cagttttatt cttgctctac cggcaccgga acagcatgg 419

<210> 309
<211> 415
<212> DNA
<213> Homo sapiens

<400> 309
ggcacgaggc tgagccagag acgccctcca ttctctcttc gcgcccgctc tccggctggc 60
ctcccgatgc gctgcccgcc ctgccaccat gacggaacag gccatctcct tcgacaaaga 120
cttcttggcc ggaggcatcg tcgccgtcat cttcaagacg gacgtggctc ctatcgagcg 180
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aagggcatcg tggactgcat tgtccgcatc cccaaagagc atggagtgct gtccttctgg 300
aagggcaacc ttgccaacgt caatcgctac ttccccactc aagccctcaa cttcgtcttc 360
aaggataatg acatgcagat cttactgggg ggcgtggaca aacacacgca ggtct 415

<210> 310
<211> 396
<212> DNA
<213> Homo sapiens

<400> 310
ggcacgagcg ggtcctgccg gtgccacatg gggtaccagg gcccgctgtg cactgactgc 60
atggacggct acttcagctc gctccggaac gagacccaca gcatctgcac agcctgtgac 120
gagtcctgca agacgtgctc gggcctgacc aacagagact gcggcgagtg tgaagtgggc 180
tgggtgctgg acgagggcgc ctgtgtggat gtggacgagt gtgcggccga gccgcctccc 240
tgcagcgctg cgcagttctg taagaacgcc aacggctcct acacgtgcga agagtgtgac 300
tccagctgtg tgggctgcac aggggaaggc ccaggaaact gtaaagagtg tatctctggc 360
tacgcgaggg agcacggaca gtgtgcagat gtggac 396

<210> 311
<211> 394
<212> DNA
<213> Homo sapiens

<400> 311
ggcacgaggc ctctgggccc tacagctcat cctggtcacg tgcccctcac tgctcgtggt 60
catgcacgtg gcctaccgcg aggaacgcga gcgcaagcac cacctgaaac acgggcccaa 120
tgccccgtcc ctgtacgaca acctgagcaa gaagcggggc ggactgtggt ggacgtactt 180
gctgagcctc atcttcaagg ccgccgtgga tgctggcttc ctctatatct tccaccgcct 240
ctacaaggat tatgacatgc cccgcgtggt ggcctgctcc gtggagcctt gcccccacac 300
tgtggactgt tacatctccc ggcccacgga gaagaaggtc ttcacctact tcatggtgac 360

cacagctgca tggagatctt cggccccagg cacc 394

<210> 312
<211> 384
<212> DNA
<213> Homo sapiens

<400> 312
ggcacgaggc gaggaacgcg agcgcaagca ccacctgaaa cacgggccca atgccccgtc 60
cctgtacgac aacctgagca agaagcgggg cggactgtgg tggacgtact tgctgagcct 120
catcttcaag gccgccgtgg atgctggctt cctctatatc ttccaccgcc tctacaagga 180
ttatgacatg ccccgcgtgg tggcctgctc cgtggagcct tgcccccaca ctgtggactg 240
ttacatctcc cggcccacgg agaagaaggt cttcacctac ttcatggtga ccacagctgc 300
catctgcatc ctgctcaacc tcagtgaagt cttctacctg gtgggcaaga ggtgcatgga 360
gatcttcggc cccaggcacc ggcg 384

<210> 313
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(430)
<223> n = A,T,C or G

<400> 313
ggcacgagcc ggctcgtaag caacctcttc agtctgcagt gggacccgcg cgtcatgcag 60
cgtgccagca gcaacctgca ccgcggtccg ggcggggcgc tggtctttct ggacaatgag 120
gcgggcttgg tgcacggcta ccgggtagca ggcatgtggg acaagtataa cgagccgctg 180
ttgcagtcag tgtgcgtgtt ccgcgagcgg accgcgcggc gcgtcctgga gctgcaccgc 240
ggacaggacg ccgcggcccg gctgctgcgc ctctaccggc gccacgagcc tcgcttcccc 300
gagctggccg cccttgcaga cccccacgct cagctgctac agcgccgcct cgacttcctc 360
gccaagcaca ttttgcactg taaggccaag tacggccgcc ggtctgggac ttagtgtcac 420
cgggaggaan 430

<210> 314
<211> 408
<212> DNA
<213> Homo sapiens

<400> 314
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ctatgacgag ttcttccccg tgtcccacgt gcgcctctgg gccctacagc tcatcctggt 120
cacgtgcccc tcactgctcg tggtcatgca cgtggcctac cgcgaggaac gcgagcgcaa 180
gcaccacctg aaacacgggc ccaatgcccc gtccctgtac gacaacctga gcaagaagcg 240
gggcggactg tggtggacgt acttgctgag cctcatcttc aaggccgccg tggatgctgg 300
cttcctctat atcttccacc gcctctacaa ggattatgac atgccccgcg tggtggcctg 360
ctccgtggag ccttgccccc acactgtgga ctgttacatc tcccggcc 408

<210> 315
<211> 412
<212> DNA
<213> homo sapiens

<400> 315
tcggagccca tgcgcagcgg ggcgcgttag ctcgcgctct tcctgacccc cgatcctggg 60
gccgaggtac ctttgacagg agcgtgaccc tgctggaggt gtgcgggagc tggcctgagg 120
gcttcgggct gcggcacatg tcctccatgg agcacacgga ggagggcctc cgggagcgac 180
ttgccgacgc catggccgag tcacctagcc gggacgtcgt gggatccgga acagaacttc 240
agcgagaggg aagcatcgag actctgagta acagctcagg ctccaccagc ggcagcatac 300
caagaaactt tgatggctac cgatctccgc tgcccaccaa tgagagccag cccctcagcc 360
tcttcccgac tggcttcccg taggtaccag caacctgctt ctgactggcc ag 412

<210> 316
<211> 300
<212> DNA
<213> homo sapiens

<400> 316
gccagcccct cagcctcttc ccgactggct tcccgtaggt accagcaacc tgcttctgac 60
tggccagccc cctcccctgc tggaggaggg gagaagcccc gctctggtcc taccccttcag 120
tctctgctct tccttcatca accaccttcc ccaagcttag tgacagcagc cgcccatcct 180
acctggatgg agaagagacc cttctccaag cacctcagcg cacttgccct ctgccacacc 240
tgtcggtgga ggctgtggcc aggagagact gtagaagctc ggtccctgtg tatgtttgca 300

<210> 317
<211> 2064
<212> DNA
<213> homo sapiens

<400> 317
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cgattttcca ggctgctatc catgtccagg gccaaacatg aatcctattg ctcttgggga 180
gccgctggct tgcttatgca gaaaacaagt tgattcgatg tcatcagtcc cgtggtggag 240
cctgtggaga caacattcag tcttatactg ccacagtcat tagtgctgct aaaacattga 300
aaagtggcct gacaatggta gggaaagtgg tgactcagct gacaggcaca ctgccttcag 360
gtgtgacaga agatgatgtt gccatccaca gtaattcacg gcggagtcct ttggtcccag 420
gcatcatcac agttattgac accgaaaccg ttggagaggg ccaggtgctt gtgagtgagg 480
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tggcttttaa tacaagtgga atgcttctag tcacaacaga caccccttggc catgactttc 600
atgtcttcca aattctgact catccttggt cctcatcaca atgtgctgtc caccatctgt 660
atactcttca caggggagaa actgaagcca aagtacagga catctgcttc agccatgact 720
gtcgctgggt tgtggtcagt actctccggg gtacttccca cgttttcccc atcaaccctt 780
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gtcgctgtag ccctgttcca ggtctatcaa gcagcccttc tgggtcaccc ttgcatggga 960
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tctctcctct tcccagcttg atggtagtga tgcctcttgc acaaatcaag cagccaatga 1080
cattggggac catcaccaaa cgaaccggca aagttaaacc tcctccacaa atttcaccca 1140
gcaaatcgat gggcggagaa ttttgtgtgg ctgctatctt cggaacatcc aggtcatggt 1200
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ccctgtacat tatcagttgc tatggcacct tagtggaaca catgatggag ccgcgacccc 1320
tcagcactgc acccaagatt agtgacgaca caccactgga aatgatgaca tcgcctcgag 1380
ccagctggac tctggttaga acccctcaat ggaatgaatt gcagccaccg tttaatgcaa 1440
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tggttccccc tggaagtcct gggcccatta ctcgacatgg gtcttacgac agtttagctt 1560
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caggccaaac cacagttatc tcatccagtt catctgtgtt gcagtctcat ggtccgagtg 1740
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tccagccagt ccgctctgac cccgtcagca tgccagggtc atcccgtcca gtctctgatc 1860
gaaggggagt ttccacagtg attgatgctg cctcaggtac ctttgacagg agcgtgaccc 1920
tgctggaggt gtgcgggagc tggcctgagg gcttcgggct gcggcacatg tcctccatgg 1980
agcacacgga ggagggcctc cgggagcgac ttgccgacgc catggccgag tcacctagcc 2040
gggacgtcgt gggatccgga acag 2064

<210> 318
<211> 1365
<212> DNA
<213> homo sapiens

<400> 318
cgagaactct gagtaacagc tcaggctcca ccagcggcag cataccaaga aactttgatg 60
gctaccgatc tccgctgccc accaatgaga gccagcccct cagcctcttc ccgactggct 120
tcccgtaggt accagcaacc tgcttctgac tggccagccc cctcccctgc tggaggaggg 180

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gagaagcccc gctctggtcc taccccttcag tctctgctct tccttcatca accaccttcc    240
ccaagcttag tgacagcagc cgcccatcct acctggatgg agaagagacc cttctccaag    300
cacctcagcg cacttgccct ctgccacacc tgtcggtgga ggctgtggcc aggagagact    360
gtagaagctc ggtccctgtg tatgtttgca tatgacatcc tgcattggat ccgcttttgt    420
attttttaac catacccacg gtggggcggg tggggggagc ctggaacagt gaccagatct    480
gggggcctga gtggggacag agttgatcgt ccacctggcc attttgaccc tgagtggaca    540
gtcacagcct cagctcatgt ctggctgtga cacacactgc ccccagcttc ccttggtcag    600
ccccactcca gcacggggtg aacggaggcc cagagtacta gggaaggagg aagggaggac    660
atgcctcttc ttcctccttt ctttccccat ctgttcctgg gaagagtttg tctttcttat    720
ctttaagccc ctttaccctg gtcctgtact gatcagtgaa ggaaaccgtg gttactgagg    780
ccctgttgaa aagtgcacgt cttgtccaat aaatcacgct gcagttggaa aaaaaaaaaa    840
aaaaaaaaag gatctttaat taagcggccg caagcttatt ccctttagtg agggttaatt    900
ttagcttggc actggccgtc gttttacaac gtcgtgactg gtaaaccctg gcgttaccca    960
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caccgatcgc ccttcccaac agttgcgcag cctgaatggc gaatgggacg cgccctgtag   1080
cggcgcatta agcgcggcgg gtgtggtggt taccgcgcag cgtgaccgct acacttgcca   1140
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